

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:49:53 ; Search time 54 Seconds
(without alignments)
261.618 Million cell updates/sec

Title: us-10-006-252a-10
Perfect score: 301
Sequence: 1 KLCERSSGTWSGVCNNAC.....QHGSNCYVPAHKICICVPPC 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep29Jan04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	301	100.0	50	2 AAW19282	AAW19282 Raphanus
2	301	100.0	50	2 AAW40350	AAW40350 Radish Rs
3	301	100.0	50	4 AAB49478	AAB49478 Radish an
4	294	97.7	50	2 AAW26384	AAW26384 Radish an
5	294	97.7	50	2 AAW26382	AAW26382 Radish an
6	293	97.3	50	2 AAW26381	AAW26381 Radish an
7	292	97.0	50	2 AAW26385	AAW26385 Radish an
8	286	95.0	50	2 AAW26383	AAW26383 Radish an
9	282	93.7	51	2 AAW19283	AAW19283 Raphanus
10	282	93.7	51	4 AAB49479	AAB49479 Radish an
11	281	93.4	51	2 AAW19281	AAW19281 Raphanus
12	281	93.4	51	2 AAW19616	AAW19616 Radish an
13	281	93.4	51	2 AAY00737	AAY00737 Antifunga
14	281	93.4	51	4 AAB67416	AAB67416 Amino aci
15	281	93.4	51	4 AAB20221	AAB20221 Radish de
16	281	93.4	51	4 AAB49471	AAB49471 Radish an
17	281	93.4	80	2 AAR33708	AAR33708 Antifunga
18	281	93.4	80	2 AAR57327	AAR57327 Antimicro
19	281	93.4	80	3 AAY91117	AAY91117 Raphanus
20	281	93.4	80	4 AAB61792	AAB61792 Radish an
21	281	93.4	149	3 AAY70323	AAY70323 Dahlia me
22	281	93.4	149	3 AAY84058	AAY84058 Amino aci
23	281	93.4	149	3 AAY84060	AAY84060 Amino aci
24	281	93.4	173	3 AAY84059	AAY84059 Amino aci
25	279	92.7	50	4 AAE10625	AAE10625 Radish pl

26	279	92.7	51	2 AAW40349	AAW40349 Radish Rs
27	279	92.7	51	2 AAY00738	AAY00738 Antifunga
28	279	92.7	51	4 AAB67417	AAB67417 Amino aci
29	279	92.7	51	4 AAB20220	AAB20220 Radish de
30	279	92.7	51	4 AAB49470	AAB49470 Radish an
31	279	92.7	51	4 AAB61793	AAB61793 White mus
32	279	92.7	80	2 AAR33706	AAR33706 Antifunga
33	279	92.7	80	2 AAR57325	AAR57325 Antimicro
34	279	92.7	80	2 AAW19280	AAW19280 Raphanus
35	279	92.7	80	2 AAW19617	AAW19617 Radish an
36	279	92.7	80	3 AAY57564	AAY57564 Wasabia j
37	279	92.7	80	5 ABP53725	ABP53725 Wasabia j
38	279	92.7	80	7 ADC51222	ADC51222 Brassica
39	279	92.7	80	7 ADC51224	ADC51224 Brassica
40	277	92.0	51	2 AAW26379	AAW26379 Radish an
41	276	91.7	51	2 AAW26387	AAW26387 Antifunga
42	275	91.4	51	2 AAW26389	AAW26389 Antifunga
43	274	91.0	51	2 AAW26386	AAW26386 Antifunga
44	274	91.0	51	2 AAW26377	AAW26377 Radish an
45	274	91.0	51	2 AAW40347	AAW40347 A. thalia

ALIGNMENTS

RESULT 1
AAW19282
ID AAW19282 standard; protein; 50 AA.
XX AC AAW19282;
XX
DT 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
DE Raphanus sativus antifungal protein 3 (RS-AFP3).
XX
KW Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defense; bacterial protection; preservative.
XX
OS Raphanus sativus.
XX
FN WO9721815-A2.
XX
PD 19-JUN-1997.
XX
PF 12-DEC-1996; 96WO-GB003068.
XX
PR 13-DEC-1995; 95GB-00025455.
PR 28-MAR-1996; 96GB-00006552.
XX
(ZENE) ZENECA LTD.
XX
PI Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX
Van Gelder WMJ;
XX
DR WPI; 1997-332786/30.
XX
PT Antifungal peptide derived from radish antifungal protein 2 - and related
PT DNA, useful for producing plants with increased fungal resistance and as
XX
therapeutic or preservative agent.
XX
PS Disclosure; Fig 1; 65pp; English.
XX
CC This protein sequence is the Raphanus sativus (radish) mature antifungal
CC protein (RS-AFP3), which is homologous to proteins AAW19280- AAW19290.
CC Shorter peptides, based on these proteins have been produced (see
CC AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW1765-834).
CC Plants containing DNA sequences encoding these proteins have improved
CC resistance to fungi. Compositions containing the peptides can be used to
CC control fungi or bacteria in pharmaceutical (e.g. treatment of Candida
CC infections) or preservative purposes (as food additives). In agriculture,
CC the peptide may be used to improve disease resistance or disease

App. priority doc

CC tolerance of crops, either pre or post harvest. When applied to plants
 CC they may also have curative as well as protective actions. The peptides
 CC may also be used to protect plants by introducing them, or a
 CC microorganism capable of expressing the peptide into the soil. (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 XX
 SQ Sequence 50 AA;

Query Match 100.0%; Score 301; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.3e-25;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLCERSGGTWSGCGNNACKNQIRLEGAQHGSNCNYVFFPAHKICICYFPC 50
 |||||
 Db 1 KLCERSGGTWSGCGNNACKNQIRLEGAQHGSNCNYVFFPAHKICICYFPC 50

RESULT 2
 AAW40350
 ID AAW40350 standard; protein; 50 AA.

XX AC AAW40350;
 XX DT 23-JUN-1998 (first entry)

DE Radish Rs-APP3 mature protein domain.

XX Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
 KW fungi; radish.

XX OS Raphanus sativus.

XX FN WO9800023-A2.

XX PD 08-JAN-1998.

XX PF 20-JUN-1997; 97WO-GB001672.

XX PR 01-JUL-1996; 96GB-00013753.

XX PA (ZONE) ZENECA LTD.

XX PI Broekaert WF, Thomma BPHJ, Penninckx IMA, Terras PRG, Manners JM;
 XX PI Kazan K;

XX DR WPI; 1998-086663/08.

XX PT Protecting plants against pathogens by inducing defensin genes - by
 PT stimulating ethylene or jasmonate pathways, also new promoter of defensin
 PT gene from Arabidopsis.

XX PS Disclosure; Fig 1C; 72pp; English.

XX CC This sequence represents the radish Rs-APP3 mature protein domain which
 CC is used to explain a novel method for the protection of plants against
 CC pathogens which involves inducing expression of a plant defensin gene by
 CC stimulating the jasmonate and/or ethylene pathways. The method is used to
 CC induce protection against necrotrophic pathogens, specifically fungi and
 CC does not require cytotoxic or potentially harmful chemicals

XX SQ Sequence 50 AA;

Query Match 100.0%; Score 301; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.3e-25;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLCERSGGTWSGCGNNACKNQIRLEGAQHGSNCNYVFFPAHKICICYFPC 50
 |||||
 Db 1 KLCERSGGTWSGCGNNACKNQIRLEGAQHGSNCNYVFFPAHKICICYFPC 50

RESULT 3
 AAB49478

ID AAB49478 standard; protein; 50 AA.

XX AC AAB49478;

XX DT 07-MAR-2001 (first entry)

XX DE Radish antifungal protein Rs-APP3.

XX KW Radish; antifungal; antimicrobial.

XX OS Raphanus sativus.

XX FN WO200071735-A1.

XX PD 30-NOV-2000.

XX PF 18-MAY-2000; 2000WO-GB001905.

XX PR 21-MAY-1999; 99GB-00011933.

XX PA (ZONE) ZENECA LTD.

XX PI Greenland AJ, Fuentes Mateos AM;

XX DR WPI; 2001-041066/05.

XX PT Antimicrobial composition useful for treating microbial diseases in
 PT plants, comprises two antimicrobial agents, which are antifungal protein
 PT from Radish and Mirabilis of Impatiens.

XX PS Disclosure; Page 26; 29pp; English.

XX CC The present sequence is an antifungal protein from Radish. This protein
 CC is useful for treating microbial diseases in plants and for inhibiting
 CC microbial growth in foodstuffs. In addition, the present sequence is
 CC useful for producing plants with improved resistance to microbial
 CC pathogens. The present protein can be used in conjunction with other
 CC antimicrobial proteins from Mirabilis (see AAB49472-B49473), and
 CC Impatiens (see AAB49474-B49477) to form an antimicrobial composition

XX SQ Sequence 50 AA;

Query Match 100.0%; Score 301; DB 4; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.3e-25;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLCERSGGTWSGCGNNACKNQIRLEGAQHGSNCNYVFFPAHKICICYFPC 50
 |||||

Db 1 KLCERSGGTWSGCGNNACKNQIRLEGAQHGSNCNYVFFPAHKICICYFPC 50
 |||||

RESULT 4
 AAW26384

ID AAW26384 standard; protein; 50 AA.

XX AC AAW26384;

XX DT 13-DEC-1997 (first entry)

XX DE Radish antifungal protein 2 mutant (delQ1.Q5M/P7S/K30G).

XX KW Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 XX preservative; transgenic plant; crop protection.

XX OS Raphanus; sativus.

XX OS Synthetic.

XX OS Chimeric.

XX PN WO9721814-A1.

XX PD 19-JUN-1997.

XX PF 12-DEC-1996; 96WO-GB003065.

Applied, mntj, doc.

XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 PA Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 DR New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 PT Disclosure; Page 4; 39pp; English.
 XX This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Glu5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX Sequence 50 AA;
 SQ Query Match 97.7%; Score 294; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 3.5e-24;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCRSSGTWGSVCGNNACKNQICIRLEGAGHGSQNYVFPFAHKICICYPPC 50
 |||||
 Db 1 KLCRSSGTWGSVCGNNACKNQICIRLEGAGHGSQNYVFPFAHKICICYPPC 50

RESULT 5
 AAW26382
 ID AAW26382 standard; protein; 50 AA.
 AC AAW26382;
 XX 13-DEC-1997 (first entry)
 DT Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/K30G/V39R).
 DE Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX WO9721814-A1.
 XX 19-JUN-1997.
 PD 12-DEC-1996; 96WO-GB003065.
 XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 PA Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 DR New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.

XX Disclosure; Page 4; 39pp; English.
 XX This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Glu5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX Sequence 50 AA;
 SQ Query Match 97.7%; Score 294; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 3.5e-24;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCRSSGTWGSVCGNNACKNQICIRLEGAGHGSQNYVFPFAHKICICYPPC 50
 |||||
 Db 1 KLCRSSGTWGSVCGNNACKNQICIRLEGAGHGSQNYVFPFAHKICICYPPC 50

RESULT 6
 AAW26381
 ID AAW26381 standard; protein; 50 AA.
 AC AAW26381;
 XX 13-DEC-1997 (first entry)
 DT Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G9R/K30G).
 DE Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX WO9721814-A1.
 XX 19-JUN-1997.
 PD 12-DEC-1996; 96WO-GB003065.
 XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 PA Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 DR New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX Disclosure; Page 4; 39pp; English.
 XX This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Glu5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to

CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX
 SQ Sequence 50 AA;

Query Match 97.3%; Score 293; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 4.5e-24;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLCERSSTWGVCGNNACKNQICIRLEGAHGSCNYVFFPAHKICICYFPC 50
 DB 1 KLCERSSTWGVCGNNACKNQICIRLEGAHGSCNYVFFPAHKICICYFPC 50

RESULT 7
 AAW26385
 ID AAW26385 standard; protein; 50 AA.

XX
 AC AAW26385;
 XX
 DT 13-DEC-1997 (first entry)

XX Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G16W/K30G).
 XX
 DE
 XX

XX Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 XX preservative; transgenic plant; crop protection.
 XX

OS Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX
 XX WO9721814-A1.

XX
 PD 19-JUN-1997.
 XX
 PF 12-DEC-1996; 96WO-GB003065.

XX
 PR 13-DEC-1995; 95GB-00025474.
 XX
 XX (ZENE) ZENECA LTD.

XX Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 XX

XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX

PS Disclosure; Page 4; 39pp; English.
 XX
 CC This polypeptide comprises a mutant isoform of radish antifungal protein

CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Gln5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1

CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX

XX Sequence 50 AA;
 Query Match 97.0%; Score 292; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 5.7e-24;

XX
 ID AAW19283
 ID AAW19283 standard; protein; 51 AA.

Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KLCERSSTWGVCGNNACKNQICIRLEGAHGSCNYVFFPAHKICICYFPC 50
 DB 1 KLCERSSTWGVCGNNACKNQICIRLEGAHGSCNYVFFPAHKICICYFPC 50

RESULT 8
 AAW26383
 ID AAW26383 standard; protein; 50 AA.

XX
 AC AAW26383;
 XX
 DT 13-DEC-1997 (first entry)

XX Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G9R/K30G/V39R).
 XX
 DE
 XX

XX Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 XX preservative; transgenic plant; crop protection.
 XX

OS Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX
 XX WO9721814-A1.

XX
 PD 19-JUN-1997.
 XX
 PF 12-DEC-1996; 96WO-GB003065.

XX
 PR 13-DEC-1995; 95GB-00025474.
 XX
 XX (ZENE) ZENECA LTD.

XX Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 XX

XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX

PS Disclosure; Page 4; 39pp; English.
 XX
 CC This polypeptide comprises a mutant isoform of radish antifungal protein

CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Gln5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1

CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX

XX Sequence 50 AA;
 Query Match 95.0%; Score 286; DB 2; Length 50;
 Best Local Similarity 96.0%; Pred. No. 2.5e-23;

XX
 ID AAW19283
 ID AAW19283 standard; protein; 51 AA.

XX
 ID AAW19283 standard; protein; 51 AA.

```
AC AAW19283;
XX
XX 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein 4 (Rs-APP4).
DE
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defensin; bacterial protection; preservative.
XX
XX Raphanus sativus.
OS
XX WO9721815-A2.
XX
XX 19-JUN-1997.
PD
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
PI Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
DR
XX Antifungal peptide derived from radish antifungal protein 2 - and related
PT DNA, useful for producing plants with increased fungal resistance and as
PT therapeutic or preservative agent.
XX
XX Disclosure; Fig 1; 65pp; English.
XX
XX This protein sequence is the Raphanus sativus (radish) mature antifungal
CC protein (Rs-APP4), which is homologous to proteins AAW19280- AAW19290.
CC Shorter peptides, based on these proteins have been produced (see
CC AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW1765-834).
CC Plants containing DNA sequences encoding these proteins have improved
CC resistance to fungi. Compositions containing the peptides can be used to
CC control fungi or bacteria in pharmaceutical (e.g. treatment of Candida
CC infections) or preservative purposes (as food additives). In agriculture,
CC the peptide may be used to improve disease resistance or disease
CC tolerance of crops, either pre or post harvest. When applied to plants
CC they may also have curative as well as protective actions. The peptides
CC may also be used to protect plants by introducing them, or a
CC microorganism capable of expressing the peptide into the soil. (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 51 AA;
SQ
Query Match 93.7%; Score 282; DB 2; Length 51;
Best Local Similarity 90.0%; Pred. No. 6.7e-23;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCRSSGTWVGCGNNACKNQICRLGAGHGSNCYVFPAAHKICYPPC 50
DB 2 KLCRSSGTWVGCGNNACKNQICINLEGARHGSCNYIFPHYRCICYPPC 51
RESULT 10
AAW19281
ID AAW19281 standard; protein; 51 AA.
XX
XX AAW19281;
AC
XX 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein 2 (Rs-APP2).
DE
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defensin; bacterial protection; preservative.
XX
XX Raphanus sativus.
OS
XX WO9721815-A2.
XX
XX 19-JUN-1997.
PD
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
PI Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
DR
```

```
OS Raphanus sativus.
XX
XX WO200071735-A1.
XX
XX 30-NOV-2000.
PD
XX 18-MAY-2000; 2000WO-GB001905.
XX
XX 21-MAY-1999; 99GB-00011933.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Greenland AJ, Fuentes Mateos AV;
PI
XX WPI; 2001-041066/05.
XX
XX Antimicrobial composition useful for treating microbial diseases in
PT plants, comprises two antimicrobial agents, which are antifungal protein
PT from Radish and Mirabilis of Impatiens.
XX
XX Disclosure; Page 26; 29pp; English.
XX
XX The present sequence is an antifungal protein from Radish. This protein
CC is useful for treating microbial diseases in plants and for inhibiting
CC microbial growth in foodstuffs. In addition, the present sequence is
CC useful for producing plants with improved resistance to microbial
CC pathogens. The present protein can be used in conjunction with other
CC antimicrobial proteins from Mirabilis (see AAB49472-B49473), and
CC Impatiens (see AAB49474-B49477) to form an antimicrobial composition
XX
XX Sequence 51 AA;
SQ
Query Match 93.7%; Score 282; DB 4; Length 51;
Best Local Similarity 90.0%; Pred. No. 6.7e-23;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCRSSGTWVGCGNNACKNQICRLGAGHGSNCYVFPAAHKICYPPC 50
DB 2 KLCRSSGTWVGCGNNACKNQICINLEGARHGSCNYIFPHYRCICYPPC 51
RESULT 11
AAW19281
ID AAW19281 standard; protein; 51 AA.
XX
XX AAW19281;
AC
XX 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein 2 (Rs-APP2).
DE
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defensin; bacterial protection; preservative.
XX
XX Raphanus sativus.
OS
XX WO9721815-A2.
XX
XX 19-JUN-1997.
PD
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
PI Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
DR
```

XX Antifungal peptide derived from radish antifungal protein 2 - and related
PT DNA, useful for producing plants with increased fungal resistance and as
PT therapeutic or preservative agent.
XX
PS Disclosure; Fig 1; 65pp; English.
XX
XX This protein sequence is the Rhanus sativus (radish) mature antifungal
CC protein (Rs-APP2), which is homologous to proteins AAW19280- AAW19290.
CC Shorter peptides, based on these proteins have been produced (see
CC AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW31765-834).
CC Plants containing DNA sequences encoding these proteins have improved
CC resistance to fungi. Compositions containing the peptides can be used to
CC control fungi or bacteria in pharmaceutical (e.g. treatment of Candida
CC infections) or preservative purposes (as food additives). In agriculture,
CC the peptide may be used to improve disease resistance or disease
CC tolerance of crops, either pre or post harvest. When applied to plants
CC they may also have curative as well as protective actions. The peptides
CC may also be used to protect plants by introducing them, or a
CC microorganism capable of expressing the peptide into the soil. (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 2; Length 51;
Best Local Similarity 92.0%; Pred. No. 8.6e-23;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCERSSTGWSGCGNNNACKNQCIRLEGAHGSQNYVFPFAHKICVYFPC 50
DB 2 KLCQSPSTGWSGCGNNNACKNQCIRLEKARHGSQNYVFPFAHKICVYFPC 51

RESULT 12
AAW19616
ID AAW19616 standard; protein; 51 AA.
XX
AC AAW19616;
XX
DT 13-DEC-1997 (first entry)
XX
DE Radish antifungal protein 2 (Rs-APP2).
XX
KW Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
KW preservative; transgenic plant; crop protection.
XX
OS Raphanus sativus.
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /note= "Gln at position 5 may be replaced by a
FT hydrophobic amino acid, preferably Met"
FT Misc-difference 9 /note= "Gly at position 9 may be replaced by a basic
FT amino acid, preferably Arg"
FT Misc-difference 16 /note= "Gly at position 16 may be replaced by a
FT hydrophobic amino acid, preferably Met"
FT Misc-difference 39 /note= "Val at position 39 may be replaced by a basic
FT amino acid, preferably Arg"
XX
PN WO9721814-A1.
XX
PD 19-JUN-1997.
XX
PF 12-DEC-1996; 96WO-GB003065.
XX
PR 13-DEC-1995; 95GB-00025474.
XX
PA (ZENE) ZENECA LTD.
XX
PI Broekaert WP, De Samblanx GW, Rees SB;

XX WPI; 1997-332785/30.
DR
XX New active mutants of radish antifungal protein 2 - used to generate
PT fungus-resistant plants or as therapeutic or preservative agents.
XX
PS Claim 1; Fig 1; 39pp; English.
XX
XX This polypeptide comprises radish antifungal protein 2 (Rs-APP2). Novel
CC potent antifungal proteins (see AAW26371-90) based on Rs-APP2 contain at
CC least 1 mutation selected from a basic residue at positions 9 or 39, and
CC a hydrophobic residue at positions 5 or 16. Proteins containing Gln5Met
CC (see AAW26379), Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg
CC (AAW26377) or Gly9Arg plus Val39Arg (AAW26378) mutations are specifically
CC claimed. A cDNA clone encoding Rs-APP2 preprotein can be modified by
CC recombinant DNA methods to allow expression of mutant isoforms in yeast
CC as mating factor alpha 1 fusion proteins. The Rs-APP2 mutants have
CC enhanced salt tolerant antifungal activity, especially when expressed in
CC plant tissue where that may have curative as well as protective effects.
CC They are useful for combating fungal diseases in agricultural,
CC pharmaceutical or preservative applications
XX
SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 2; Length 51;
Best Local Similarity 92.0%; Pred. No. 8.6e-23;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCERSSTGWSGCGNNNACKNQCIRLEGAHGSQNYVFPFAHKICVYFPC 50
DB 2 KLCQSPSTGWSGCGNNNACKNQCIRLEKARHGSQNYVFPFAHKICVYFPC 51

RESULT 13
AAW00737
ID AAW00737 standard; peptide; 51 AA.
XX
AC AAW00737;
XX
DT 14-MAY-1999 (first entry)
XX
DE Antifungal peptide RsAPP2.
XX
KW Antifungal agent; food additive; food spoilage prevention.
XX
OS Synthetic.
XX
PN WO9902038-A1.
XX
PD 21-JAN-1999.
XX
PF 09-JUL-1998; 98WO-GB002010.
XX
PR 10-JUL-1997; 97GB-00014564.
XX
PA (ZENE) ZENECA LTD.
XX
PI Greenland AJ, Fuentes Mateos AM;
XX
XX WPI; 1999-120402/10.
DR
XX Food additive synergistically enhances activity of an antifungal agent -
PT especially for prevent food and beverage spoilage.
XX
PS Claim 15; Fig 7; 40pp; English.
XX
XX This sequence represents an antifungal peptide. The invention relates to
CC an antifungal composition comprising one or more antifungal agents and
CC one or more food additives, providing that the composition does not
CC contain nicin or lactoferrin or a derivative, trichorizamine or lysozyme,
CC the relative amounts of antifungal agent and food additive being such
CC that they enhance the activity of the overall antifungal activity of the
CC composition. Especially the antifungal agent is derived from a plant or

CC seed and the food additive is selected from an acid, salt or ester or a 1
 CC -6C alkyl ether or derivatives. The compositions are useful in preventing
 CC food spoilage e.g. in a wide range of foods and beverages including
 CC fruits, jams and dairy products, caused by the spoilage organisms
 CC *Fusarium culmorum*, *Penicillium chrysogenum*, *P. roquefortii*, *P.*
 CC *nauligovense*, *P. commune*, *Alternaria* sp., *Cladosporium* sp., *Tichoderma*
 CC *harzianum*, *Mucor plumbeus*, *Aspergillus versicolor* and *Scopulariopsis*
 CC *brevicaulis*. The food additive and antifungal agent act synergistically
 CC to enhance the overall antifungal activity of the composition to a level
 CC above the sum of each single component
 XX
 SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 2; Length 51;
 Best Local Similarity 92.0%; Pred. No. 8.6e-23;
 Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCRSSTGWSGVCNNACKQCIRLEGAQHGSNNYVPPAHKCIYPPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 KLCQPSGTWSGVCNNACKQCIRLEKARHGSCNNYVPPAHKCIYPPC 51

RESULT 14
 AAB67416
 ID AAB67416 standard; protein; 51 AA.

XX AAB67416;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Amino acid sequence of the plant defensin Rs-APP2.

XX Defensin; antimicrobial; microbial infection; fungal infection;
 XX pathogenic fungi; bacterial infection; transgenic plant;
 XX microbial pathogen; fungal resistance.

XX *Raphanus sativus*.
 OS
 PN WO200109175-A2.

XX 08-FEB-2001.

XX 31-JUL-2000; 2000WO-GB002968.

XX 02-AUG-1999; 99GB-00018156.

XX (ZENE-) ZENEGA LTD.

XX Posthuma GA, Schaaper WM, Sijtsma L, Van Amerongen A, Fant F;
 PI Borremans FAM, Rees SB, Osborn RW;

XX WPI; 2001-182939/18.

XX Antimicrobial peptide for combating bacterial infections, comprises
 PT modified cysteine residues, modified by addition, substitution or
 PT deletion to block their ability to form disulfide bridges.

XX Disclosure; Page 3; 45pp; English.

XX The present sequence represents a plant defensin protein. Defensins
 CC have antimicrobial properties. The specification describes a modified Cys
 CC -containing antimicrobial peptide derived from a plant defensin. The
 CC peptide is modified by introducing one or more Cys residues and/or
 CC replacing or altering one or more Cys residues to block their ability to
 CC form disulfide bridges. The antimicrobial peptide is useful in the
 CC treatment and prevention of microbial infections e.g. for combating
 CC fungal infection. It is useful for agricultural and pharmaceutical
 CC applications. It is also useful against a broad spectrum of pathogenic
 CC fungi and is also useful in combating bacterial infections. A DNA
 CC sequence encoding the antimicrobial peptide is useful for producing
 CC transgenic plants with increased resistance to microbial pathogen, such
 CC that the plant is used as a parent in standard plant breeding crosses to
 CC develop hybrids and lines having improved fungal resistance

XX SQ Sequence 51 AA;
 Query Match 93.4%; Score 281; DB 4; Length 51;
 Best Local Similarity 92.0%; Pred. No. 8.6e-23;
 Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KLCRSSTGWSGVCNNACKQCIRLEGAQHGSNNYVPPAHKCIYPPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 KLCQPSGTWSGVCNNACKQCIRLEKARHGSCNNYVPPAHKCIYPPC 51

RESULT 15

AAB20221
 ID AAB20221 standard; protein; 51 AA.

XX AAB20221;

XX 14-MAY-2001 (first entry)

XX Radish defensin Rs-APP2.

XX Radish; defensin; Rs-APP2; antimicrobial; antifungal; fungicide;
 XX transgenic plant; disease resistance; infection; therapy.

XX *Raphanus sativus*.

XX Key Location/Qualifiers

FT Disulfide-bond 4..51

FT Disulfide-bond 15..36

FT Disulfide-bond 21..45

FT Disulfide-bond 25..47

FT Misc-difference 32

FT /note= "optionally substituted by Trp in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 34

FT /note= "optionally substituted by Val, Leu, Ile, Trp,

FT Phe, Lys, Arg, Tyr, Met, Cys or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 35

FT /note= "optionally substituted by Ile, Trp, Lys, Arg,

FT Val, Leu, Phe, His in antimicrobial protein/peptide of

FT Claim 1"

FT Misc-difference 36

FT /note= "optionally substituted by Trp in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 37

FT /note= "optionally substituted by Trp, Gly, Thr, Tyr,

FT Gln, Lys, Arg, Phe or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 38

FT /note= "optionally substituted by Leu, Ile, Trp, Phe,

FT Val, Cys in antimicrobial protein/peptide of Claim 1"

FT Misc-difference 39

FT /note= "optionally substituted by Leu, Ile, Trp, Phe,

FT Met, Lys, Arg, Tyr or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 40

FT /note= "optionally substituted by Trp in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 41

FT /note= "optionally substituted by Ile, Trp, Phe, Ser,

FT Thr, Tyr, Gln, Asn, Lys, Arg or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 42

FT /note= "optionally substituted by Val, Leu, Ile, Trp,

FT Phe, Tyr, Asn, Lys, Arg, Ser or Thr in antimicrobial

FT protein/peptide of Claim 1"

XX WO200109174-A2.

XX 08-FEB-2001.

XX

Search completed: May 11, 2004, 16:56:27
Job time : 55 secs

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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:55:24 ; Search time 23 Seconds
(without alignments)
112.230 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCRSSGTSWGVCGNNAC.....QHGSNCYVFAHKICVFPFC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/2/iaa/5A-COMB.pep.*
- 2: /cgn2_6/prodata/2/iaa/5B-COMB.pep.*
- 3: /cgn2_6/prodata/2/iaa/6A-COMB.pep.*
- 4: /cgn2_6/prodata/2/iaa/6B-COMB.pep.*
- 5: /cgn2_6/prodata/2/iaa/ACTUS-COMB.pep.*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	301	100.0	50	4	US-09-077-951-10
2	301	100.0	50	4	US-09-077-948A-36
3	294	97.7	50	4	US-09-077-951-68
4	294	97.7	50	4	US-09-077-951-70
5	293	97.3	50	4	US-09-077-951-67
6	292	97.0	50	4	US-09-077-951-71
7	286	95.0	50	4	US-09-077-951-69
8	282	93.7	51	4	US-09-077-951-11
9	282	93.7	51	4	US-09-077-948A-37
10	281	93.4	51	1	US-08-656-318A-4
11	281	93.4	51	1	US-08-627-706-19
12	281	93.4	51	2	US-08-956-459-4
13	281	93.4	51	3	US-09-103-489-19
14	281	93.4	51	4	US-09-077-951-9
15	281	93.4	51	4	US-09-077-951-20
16	281	93.4	51	4	US-09-077-951-37
17	281	93.4	51	4	US-09-077-951-77
18	281	93.4	51	4	US-09-077-948A-35
19	281	93.4	51	4	US-09-829-381D-19
20	281	93.4	80	1	US-08-377-687-59
21	281	93.4	80	2	US-08-777-193-59
22	281	93.4	80	3	US-08-971-983-59
23	281	93.4	80	4	US-09-589-733C-21
24	279	92.7	51	1	US-08-377-687-19
25	279	92.7	51	1	US-08-656-318A-3
26	279	92.7	51	1	US-08-627-706-18
27	279	92.7	51	2	US-08-777-192-19

28	279	92.7	51	2	US-08-956-459-3	Sequence 3, Appl
29	279	92.7	51	3	US-08-971-982-19	Sequence 19, Appl
30	279	92.7	51	3	US-09-103-489-18	Sequence 18, Appl
31	279	92.7	51	4	US-09-077-951-8	Sequence 8, Appl
32	279	92.7	51	4	US-09-077-948A-34	Sequence 34, Appl
33	279	92.7	51	4	US-09-829-381D-18	Sequence 18, Appl
34	279	92.7	51	4	US-09-589-733C-22	Sequence 22, Appl
35	279	92.7	80	1	US-08-377-687-49	Sequence 49, Appl
36	279	92.7	80	2	US-08-777-192-49	Sequence 49, Appl
37	279	92.7	80	3	US-08-971-982-49	Sequence 49, Appl
38	279	92.7	80	3	US-09-103-489-20	Sequence 20, Appl
39	279	92.7	80	4	US-09-829-381D-20	Sequence 20, Appl
40	277	92.0	51	4	US-09-077-951-22	Sequence 22, Appl
41	277	92.0	51	4	US-09-077-951-29	Sequence 29, Appl
42	277	92.0	51	4	US-09-077-951-65	Sequence 65, Appl
43	276	91.7	51	4	US-09-077-951-31	Sequence 31, Appl
44	276	91.7	51	4	US-09-077-951-39	Sequence 39, Appl
45	276	91.7	51	4	US-09-077-951-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-077-951-10
; Sequence 10, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PP050093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-10

Query Match 100.0%; Score 301; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLCRSSGTSWGVCGNNACNQICIRLEGAGHSCNYVFAHKICVFPFC 50
Db 1 KLCRSSGTSWGVCGNNACNQICIRLEGAGHSCNYVFAHKICVFPFC 50

RESULT 2
US-09-077-948A-36
; Sequence 36, Application US/09077948A
; Patent No. 6605698
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Sitjtsma, Iolke
; APPLICANT: Meloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins

priority due.

priority due.

; FILE REFERENCE: 109846-257 (SYN-035)
; CURRENT APPLICATION NUMBER: US/09/077,948A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-948A-36

Query Match 100.0%; Score 301; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50

RESULT 3

US-09-077-951-68
; Sequence 68, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-68

Query Match 97.7%; Score 294; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 3.7e-25;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50

RESULT 4

US-09-077-951-70
; Sequence 70, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13

; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-70

Query Match 97.7%; Score 294; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 3.7e-25;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50

RESULT 5

US-09-077-951-67
; Sequence 67, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-67

Query Match 97.3%; Score 293; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 4.7e-25;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50

RESULT 6

US-09-077-951-71
; Sequence 71, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 50
; TYPE: PRT


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; ORGANISM: Raphanus sativus
US-09-077-951-71

Query Match          97.0%; Score 292; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 6e-25;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCRSSTGWSGVCNNACKNQCIRLEGAQHGSNCNVFFPAHKICICYFPC 50
DB 1 KLCRSSTGWSGVCNNACKNQCIRLEGAQHGSNCNVFFPAHKICICYFPC 50

RESULT 7
US-09-077-951-69
; Sequence 69, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 69
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-69

Query Match          95.0%; Score 286; DB 4; Length 50;
Best Local Similarity 96.0%; Pred. No. 2.7e-24;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 KLCRSSTGWSGVCNNACKNQCIRLEGAQHGSNCNVFFPAHKICICYFPC 50

RESULT 8
US-09-077-951-11
; Sequence 11, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-11

Query Match          93.7%; Score 282; DB 4; Length 51;
Best Local Similarity 90.0%; Pred. No. 7.4e-24;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-627-706-19

Query Match          93.4%; Score 281; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 9.4e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCRRSGTSGVCGNNAACKNCQIRLEGAQHGSNCYVFPFAHKICICYPPC 50
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Db 2 KLCRPSGTSGVCGNNAACKNCQIRLEKARHGSNCYVFPFAHKICICYPPC 51

RESULT 12
US-08-956-459-4
; Sequence 4, Application US/08956459
; Patent No. 5919918
; GENERAL INFORMATION:
; APPLICANT: BROEKART, WILLEM F.
; APPLICANT: CAMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,459
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/656,318
; FILING DATE: 12-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02766
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326424.0
; FILING DATE: 24-DEC-1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Rs-AFP2
US-08-956-459-4

Query Match          93.4%; Score 281; DB 2; Length 51;
Best Local Similarity 92.0%; Pred. No. 9.4e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCRRSGTSGVCGNNAACKNCQIRLEGAQHGSNCYVFPFAHKICICYPPC 50
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Db 2 KLCRPSGTSGVCGNNAACKNCQIRLEKARHGSNCYVFPFAHKICICYPPC 51

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:56:34 ; Search time 42 Seconds
(without alignments)
330.437 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCRSSGTWVGCGNNAC.....QHGSNYYVFAHKICVFFC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pcp.*
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- 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	301	100.0	50	9	US-09-732-561-20
2	301	100.0	50	12	US-10-388-361A-36
3	301	100.0	50	13	US-10-006-252A-10
4	294	97.7	50	13	US-10-006-252A-68
5	294	97.7	50	13	US-10-006-252A-70
6	293	97.3	50	13	US-10-006-252A-67
7	292	97.0	50	13	US-10-006-252A-71
8	286	95.0	50	13	US-10-006-252A-69
9	282	93.7	51	12	US-10-388-361A-37
10	282	93.7	51	13	US-10-006-252A-11
11	281	93.4	51	9	US-09-829-381A-19
12	281	93.4	51	12	US-10-681-972-19
13	281	93.4	51	12	US-10-388-361A-35
14	281	93.4	51	13	US-10-006-252A-9
15	281	93.4	51	13	US-10-006-252A-20

16	281	93.4	51	13	US-10-006-252A-37
17	281	93.4	51	13	US-10-006-252A-77
18	281	93.4	51	15	US-10-072-809A-34
19	281	93.4	80	9	US-09-759-584-59
20	281	93.4	80	12	US-10-636-396-21
21	279	92.7	51	9	US-09-759-584-19
22	279	92.7	51	9	US-09-732-561-19
23	279	92.7	51	9	US-09-823-381A-18
24	279	92.7	51	12	US-10-681-972-18
25	279	92.7	51	12	US-10-388-361A-34
26	279	92.7	51	12	US-10-636-396-22
27	279	92.7	51	13	US-10-006-252A-8
28	279	92.7	51	15	US-10-072-809A-33
29	279	92.7	51	15	US-10-072-809A-35
30	279	92.7	80	9	US-09-759-584-49
31	279	92.7	80	9	US-09-829-381A-20
32	279	92.7	80	12	US-10-681-972-20
33	277	92.0	51	13	US-10-006-252A-22
34	277	92.0	51	13	US-10-006-252A-29
35	277	92.0	51	13	US-10-006-252A-65
36	276	91.7	51	13	US-10-006-252A-31
37	276	91.7	51	13	US-10-006-252A-39
38	276	91.7	51	13	US-10-006-252A-44
39	276	91.7	51	13	US-10-006-252A-73
40	275	91.4	51	13	US-10-006-252A-28
41	275	91.4	51	13	US-10-006-252A-41
42	275	91.4	51	13	US-10-006-252A-42
43	275	91.4	51	13	US-10-006-252A-75
44	274	91.0	51	9	US-09-732-561-17
45	274	91.0	51	13	US-10-006-252A-23

ALIGNMENTS

RESULT 1

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; Sequence 20, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
;   APPLICANT: Thoma, Bart
;   APPLICANT: Terras, Franky
;   APPLICANT: Penninckx, Iris
;   APPLICANT: Manners, John
;   APPLICANT: Kazan, Kemal
;   APPLICANT: Broekaert, Willem
;   TITLE OF INVENTION: Plant Protection Method
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ZENECA AG Products
;   STREET: 1800 Concord Pike
;   CITY: Wilmington
;   STATE: DE
;   COUNTRY: USA
;   ZIP: 19850
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/732,561
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/202,638
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB97/01672
;   FILING DATE: 20-JUN-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Hohenschutz, Liza D.
;   REGISTRATION NUMBER: 33,712

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; Sequence 70, Application US/100062522
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah

```

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; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-70

Query Match          97.7%; Score 294; DB 13; Length 50;
Best Local Similarity 98.0%; Pred. No. 5.7e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 KLCMRSSGTWSGVCNNACKKQCIIRLEGAQHGSNNYVPPAHKICICYFPC 50

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RESULT 6
US-10-006-252A-67
; Sequence 67, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-67

Query Match          97.3%; Score 293; DB 13; Length 50;
Best Local Similarity 98.0%; Pred. No. 7.3e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 KLCMRSSGTWSGVCNNACKKQCIIRLEGAQHGSNNYVPPAHKICICYFPC 50

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RESULT 7
US-10-006-252A-71
; Sequence 71, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A

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; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-71

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Best Local Similarity 98.0%; Pred. No. 9.5e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 KLCMRSSGTWSGVCNNACKKQCIIRLEGAQHGSNNYVPPAHKICICYFPC 50

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RESULT 8
US-10-006-252A-69
; Sequence 69, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-69

Query Match          95.0%; Score 286; DB 13; Length 50;
Best Local Similarity 96.0%; Pred. No. 4.5e-25;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 KLCMRSSGTWSGVCNNACKKQCIIRLEGAQHGSNNYVPPAHKICICYFPC 50

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RESULT 9
US-10-388-361A-37
; Sequence 37, Application US/10388361A
; Publication No. US20030226169A1
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Sitjtsma, Lolke
; APPLICANT: Meloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem

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APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PPDDIV
CURRENT APPLICATION NUMBER: US/10/388.361A
PRIOR FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: US 09/077,948
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR FILING DATE: 1996-03-28
PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 51
TYPE: PRT
ORGANISM: Raphanus sativus
US-10-388-361A-37

Query Match 93.7%; Score 282; DB 12; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.3e-24;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAOHGSCNYVFFPAHKICICYPC 50
Db 2 KLCERSGTWSGVCNNACKNQICIRLEGAOHGSCNYVFFHRCICICYPC 51

RESULT 10
US-10-006-252A-11
Sequence 11, Application US/10006252A
Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-07-951
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1995-12-13
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 51
TYPE: PRT
ORGANISM: Raphanus sativus
US-10-006-252A-11

Query Match 93.7%; Score 282; DB 13; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.3e-24;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAOHGSCNYVFFPAHKICICYPC 50
Db 2 KLCERSGTWSGVCNNACKNQICIRLEGAOHGSCNYVFFHRCICICYPC 51

RESULT 11
US-09-829-381A-19
Sequence 19, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.

Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, B34F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-829-381A-19

Query Match 93.4%; Score 281; DB 9; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAOHGSCNYVFFPAHKICICYPC 50
Db 2 KLCQRFSGTWSGVCNNACKNQICIRLEKARHGSCNYVFFPAHKICICYPC 51

RESULT 12
US-10-681-972-19
Sequence 19, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
Controlling Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 51
TYPE: PRT


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; ORGANISM: Raphanus sativus
US-10-691-972-19

Query Match      93.4%; Score 281; DB 12; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 2 KLCQRPSTGWSGVCNNACKNQICIRLEKARHGSCNYVPPAHKCIYFPC 51

RESULT 13
US-10-388-361A-35
; Sequence 35, Application US/10388361A
; Publication No. US20030226169A1
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Pant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Sitjtsma, Lolke
; APPLICANT: Melloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; FILE OF INVENTION: Antifungal Proteins
; CURRENT APPLICATION NUMBER: US/10/388,361A
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 09/077,948
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-388-361A-35

Query Match      93.4%; Score 281; DB 12; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCRSSGTWSGVCNNACKNQICIRLEGAHQSCNYVPPAHKCIYFPC 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 KLCQRPSTGWSGVCNNACKNQICIRLEKARHGSCNYVPPAHKCIYFPC 51

RESULT 14
US-10-006-252A-9
; Sequence 9, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; FILE OF INVENTION: Antifungal Proteins
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13

; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-9

Query Match      93.4%; Score 281; DB 13; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCRSSGTWSGVCNNACKNQICIRLEGAHQSCNYVPPAHKCIYFPC 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 KLCQRPSTGWSGVCNNACKNQICIRLEKARHGSCNYVPPAHKCIYFPC 51

Search completed: May 11, 2004, 17:00:01
Job time : 56 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 16:54:24 ; Search time 20 Seconds
(without alignments)
240.479 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCERSSGTWSGCGNNAC.....QHGSNCYVFPAAKICICYPC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	301	100.0	79	2 T10243	antifungal protein
2	301	100.0	79	2 T07917	antifungal protein
3	282	93.7	80	2 T10183	antifungal protein
4	281	93.4	80	2 T10823	antifungal protein
5	279	92.7	80	2 T0176	antifungal protein
6	279	92.7	80	2 T02622	probable antifunga
7	274	91.0	80	2 F96787	protein T4O12.7 [i
8	272	90.4	80	2 T02621	probable antifunga
9	167	55.5	56	2 G86328	hypothetical prote
10	162	53.8	50	2 S66221	defensin AMP1 - Da
11	151	50.2	30	2 S28991	antifungal protein
12	145	48.2	161	2 S12246	anther-specific pr
13	142	47.2	27	2 S28989	antifungal protein
14	140.5	46.7	49	2 S66219	defensin AMP1 - C1
15	138	45.8	25	2 S28993	antifungal protein
16	137	45.5	27	2 S28995	antifungal protein
17	136	45.2	26	2 S28994	antifungal protein
18	134.5	44.7	54	2 S66220	defensin APp1 - He
19	134	44.5	27	2 S28990	antifungal protein
20	129.5	43.0	50	2 S66218	defensin AMP1 - Ae
21	116.5	38.7	80	2 F96591	probable gamma-thi
22	116.5	38.7	83	2 T14866	probable gamma-thi
23	105.5	35.0	182	2 S46272	anther-specific pr
24	101.5	33.7	93	2 T03673	piti protein (Clon
25	82.5	27.4	105	2 S57809	gamma-thionin-like
26	80.5	26.7	55	2 D96636	unknown protein, 8
27	77.5	25.7	47	2 A58319	gamma-zeathionin 1
28	75.5	25.1	47	2 S11529	gamma-purothionin
29	75.5	25.1	105	2 S23574	thionin precursor,

30	74.5	24.8	47	2 S69146	gamma-thionin Si-a
31	74.5	24.8	47	2 S13849	hordothionin gamma
32	74.5	24.8	47	2 S69144	gamma-thionin Si-a
33	74	24.6	1408	2 S16148	gene serrate prote
34	73.5	24.4	2233	2 T28669	surface protein 51
35	73	24.3	64	1 NTSR3B	neurotoxin III - s
36	73	24.3	85	1 NTSR2A	neurotoxin II prec
37	72.5	24.1	73	2 D84433	proteinase inhibit
38	72	23.9	20	2 S66222	defensin AMP2 - Da
39	71.5	23.8	81	2 T02667	proteinase inhibit
40	70.5	23.4	72	2 T06599	disease resistance
41	70.5	23.4	82	2 JC7897	defensin 1 precurs
42	70.5	23.4	1394	2 A35626	transforming growt
43	70	23.3	74	2 T06766	disease resistance
44	69.5	23.1	47	2 S11530	purothionin gamma
45	69	22.9	65	1 NTSREB	neurotoxin XI - sc

ALIGNMENTS

RESULT 1

T10243

antifungal protein 3 precursor - radish

C/Species: Raphanus sativus (radish)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000

C/Accession: T10243

R/Terras, F.R.G.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.

submitted to the EMBL Data Library, April 1996

A/Reference number: Z16994

A/Accession: T10243

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-79 <TER>

A/Cross-references: EMBL:X97319

A/Experimental source: cultivar Ronde Rode Kleine Witpunt

C/Genetics:

A/Gene: AFP3

C/Superfamily: gamma-thionin

C/Keywords: antifungal

C/Keywords: signal sequence #status predicted <SIG>

F;1-29/Domain: signal sequence #status predicted <SIG>

F;30-79/Product: antifungal protein 3 #status predicted <MAT>

Query Match 100.0%; Score 301; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLCERSSGTWSGCGNNACNQCIRLEGAQHGSNCYVFPAAKICICYPC 50
Db 30 KLCERSSGTWSGCGNNACNQCIRLEGAQHGSNCYVFPAAKICICYPC 79

RESULT 2

T07917

antifungal protein - rape

C/Species: Brassica napus (rape)

C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jun-2000

C/Accession: T07917

R/Sohn, U.; Lee, C.M.; Lee, M.H.; Kim, J.H.

submitted to the EMBL Data Library, May 1996

A/Reference number: Z16214

A/Accession: T07917

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-79 <SOH>

A/Cross-references: EMBL:U59459; NID:gl399229; PIDN:AAB03224.1; PID:gl399230

A/Experimental source: cv. Naehan

C/Superfamily: gamma-thionin

Query Match 100.0%; Score 301; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 50
|||||
Db 30 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 79
|||||

RESULT 3

T10183
antifungal protein 4 precursor - radish
C;Species: Raphanus sativus (radish)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T10183
R;Terras, F.R.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z1981
A;Accession: T10183
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-80 <TER>
A;Cross-references: EMBL:X97318
A;Experimental source: cultivar Ronde Kleine Witpunt
C;Genetics:
A;Gene: AFP4
C;Superfamily: gamma-thionin
C;Keywords: antifungal
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-80/Product: antifungal protein 4 #status predicted <MAT>

Query Match 93.7%; Score 282; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 2.5e-23;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 50
|||||
Db 31 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 80
|||||

RESULT 4

T10823
antifungal protein 2 precursor - radish
C;Species: Raphanus sativus (radish)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C;Accession: T10823; B42842
R;Terras, F.R.; Eggermont, K.; Kovaleva, V.; Raikhel, N.V.; Osborn, R.W.; Kester, A.; Re
Plant Cell 7, 568-573, 1995
A;Title: Small cysteine-rich antifungal proteins from radish: their role in host defense
A;Reference number: Z19976
A;Accession: T10823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-80 <TER>
A;Cross-references: EMBL:U18556; NID:g609319; PID:g609320
A;Experimental source: seed
R;Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden,
J. Biol. Chem. 267, 15301-15309, 1992
A;Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanu
A;Reference number: A42842; MUID:92348373; PMID:1639777
A;Accession: B42842
A;Status: preliminary
A;Molecule type: protein
A;Residues: 30-65 <TE2>
A;Experimental source: seed
A;Note: sequence extracted from NCBI backbone (NCBIP:109572)
C;Genetics:
A;Gene: AFP2
C;Function:
A;Description: has antifungal activity
C;Superfamily: gamma-thionin
F;1-43/Domain: signal sequence #status predicted <SIG>
F;44-80/Product: antifungal protein 2 #status predicted <MAT>

Query Match 93.4%; Score 281; DB 2; Length 80;
Best Local Similarity 92.0%; Pred. No. 3.2e-23;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 50
|||||
Db 31 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 80
|||||

RESULT 5

T10176
antifungal protein 1 precursor - radish
C;Species: Raphanus sativus (radish)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C;Accession: T10176; A42842
R;Terras, F.R.; Eggermont, K.; Kovaleva, V.; Raikhel, N.V.; Osborn, R.W.; Kester, A.; Re
Plant Cell 7, 568-573, 1995
A;Title: Small cysteine-rich antifungal proteins from radish: their role in host defense.
A;Reference number: Z16976
A;Accession: T10176
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-80 <TER>
A;Cross-references: EMBL:U18557; NID:g644773; PID:g609322
A;Experimental source: strain ronde rode kleine witpunt; tissue type seed
R;Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden,
J. Biol. Chem. 267, 15301-15309, 1992
A;Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanu
A;Reference number: A42842; MUID:92348373; PMID:1639777
A;Accession: A42842
A;Status: preliminary
A;Molecule type: protein
A;Residues: 30-73 <TE2>
A;Experimental source: seed
C;Genetics:
A;Gene: AFP1
C;Function:
A;Description: involved in creation of a microenvironment around the seed in which fungal
A;Note: preferentially released during seed germination
C;Superfamily: gamma-thionin
C;Keywords: antifungal
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-80/Product: antifungal protein 1 #status predicted <MAT>

Query Match 92.7%; Score 279; DB 2; Length 80;
Best Local Similarity 92.0%; Pred. No. 5.2e-23;
Matches 46; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 50
|||||
Db 31 KLCERSGTWVGCGNNACKNQICIRLEGAOHGSCNYYVFFPAHKICICYFPC 80
|||||

RESULT 6

T02622
probable antifungal protein T19L18.18 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02622; D84655
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A;Reference number: Z14681
A;Accession: T02622
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-80 <ROU>
A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413711
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: D84655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE002093; NID:g3413711; PIDN:AAC31234.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g26010; T19L18.18
 A;Map position: 2
 A;Introns: 22/1
 C;Superfamily: gamma-thionin

Query Match 92.7%; Score 279; DB 2; Length 80;
 Best Local Similarity 90.0%; Pred. No. 5.2e-23;
 Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCERSGTWGVCGNNACKNQICIRLEGAQHGSNCYVFFPAHKICICYFPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 31 KLCRKPSGTWGVCGNSACKNQICINLEGAKEHGSNCYVFFPAHKICICYFPC 80

RESULT 7

F96787
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C;Accession: F96787
 R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F96787
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE005173; NID:g6721100; PIDN:AAF26754.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: T4012.7
 A;Map position: 1
 C;Superfamily: gamma-thionin

Query Match 91.0%; Score 274; DB 2; Length 80;
 Best Local Similarity 90.0%; Pred. No. 1.8e-22;
 Matches 45; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLCERSGTWGVCGNNACKNQICIRLEGAQHGSNCYVFFPAHKICICYFPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 31 KLCRKPSGTWGVCGNSACKNQICINLEKARHGSNCYVFFPAHKICICYFPC 80

RESULT 8

T02621
 Probable antifungal protein T19L18.17 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
 C;Accession: T02621; E84655
 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, August 1998
 A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
 A;Reference number: Z14681
 A;Accession: T02621
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-80 <ROU>
 A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413721
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: E84655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE002093; NID:g3413721; PIDN:AAC31244.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g26020; T19L18.17
 A;Map position: 2
 A;Introns: 22/1
 C;Superfamily: gamma-thionin

Query Match 90.4%; Score 272; DB 2; Length 80;
 Best Local Similarity 88.0%; Pred. No. 2.9e-22;
 Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLCERSGTWGVCGNNACKNQICIRLEGAQHGSNCYVFFPAHKICICYFPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 31 KLCRKPSGTWGVCGNSACKNQICINLEGAKEHGSNCYVFFPAHKICICYFPC 80

RESULT 9

G86328
 Hypothetical protein F14P1.6 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C;Accession: G86328
 R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,
 Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G86328
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-56 <STO>
 A;Cross-references: GB:AE005172; NID:g9795584; PIDN:AAF98402.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 55.5%; Score 167; DB 2; Length 56;
 Best Local Similarity 52.0%; Pred. No. 3.2e-11;
 Matches 26; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 KLCERSGTWGVCGNNACKNQICIRLEGAQHGSNCYVFFPAHKICICYFPC 50
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 7 RICERSKTWTGFCGTRGCDSDCKRWERASHGACHAQPFGFACFCYFNC 56

RESULT 10

S66221
 defensin AMP1 - Dahlia merckii
 N;Alternate names: seed antifungal protein
 C;Species: Dahlia merckii
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
 C;Accession: S66221
 R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Le,
 FEBS Lett. 368, 257-262, 1995
 A;Title: Isolation and characterisation of plant defensins from seeds of Asteraceae,
 A;Reference number: S66218; MUID:95354848; PMID:7628617
 A;Accession: S66221
 A;Molecule type: protein
 A;Residues: 1-50 <OSB>

C;Keywords: antifungal

Query Match 53.8%; Score 162; DB 2; Length 50;
Best Local Similarity 54.0%; Pred. No. 9.9e-11;
Matches 27; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Qy		1 KLCERSSTGWSVCGNNACKNQICIRLEGAQHGSNCNVFPFAHKCIYFPC	50
	:	:	:
Dh	1 ELCEKASKTWSVCGNTGHCDNCKSWEGAAGHAGACHVRNGKHMCFCYENC	50	

RESULT 11

RESOL 11
S28991
antifungal protein 1 - rape (fragment)

C;Species: *Brassica napus* (rape)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S28991 S28992
R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, E.A.; A:Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
A;Reference number: S28989 MIMD:93138130 PMID:8422949

A:Accession: S28991
A:Molecule type: protein
A:Residues: 1-30 <TE1>
A:Accession: S28992
A:Molecule type: protein
A:Residues: 1-23 <TE2>
C:Superfamily: gamma-thionin

Query Match 50.2%; Score 151; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 9.8e-10;
Matches 26; Conservative 0; Mismatches 2; Indels

Qy	1	KLCERSSTGTSWGVCGNNACNQCIRLE	28
Db	2	KLCERPSTGTSWGVCGNNACNOCINLE	29

RESULT 12

another-specific protein SF18 precursor - common sunflower (fragment)
 C:Species: Helianthus annuus (common sunflower)
 C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 15-Sep-2003
 C:Accession: S12246
 R:Donor, C.: Eyrard, J.L.: Herdenberger, F.; Pillay, D.T.N.; Steinmetz, A.
 Plant Mol. Biol. 15, 643-646, 1990
 A:Title: Nucleotide sequence of two anther-specific cDNAs from sunflower (Helianthus annuus) anther-specific protein SF18
 A:Reference number: S12245; MUID:91338702; PMID:2102380
 A:Accession: S12246
 A:Molecule type: mRNA
 A:Residues: 1-161 <DOM>
 A:Cross-references: EMBL:X53375; NID:gl18812; PIDN:CAA37455.1; PID:gl18813
 F:1-8/Domain: signal sequence (fragment) #status predicted <SIG>
 F:9-161/Product: anther-specific protein SF18 #status predicted <MAT>

Query Match 48.2%; Score 145; DB 2; Length 161;
Best Local Similarity 46.0%; Pred. No. 1.6e-08;
Matches 23; Conservative 8; Mismatches 19; Indels 0; Gaps

```
QY      1 KLCERSGTTWGVCGNNNACKNQIRLEGAHGSCNVFPAHKCIYCYPFC 50  
        :|::||| |:| ::|||::|::| |::| |::|  
Db     16 KICEKSKTWFGNCXDTDKCDKRICDWEAGKHGACHOREAKHMCFCYFDC 65
```

PRECIPIT. T 13

RES001_13
 528169
 C:Antifungal protein 1 - turnip (fragment)
 C:Antifungal Brassica rapa (turnip)
 C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
 C:Accession: S28989
 C:Terminator: F.R.G.; Torrekens, S.; van Leeuwen, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, E.A.; Aelter, A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
 FEBS Lett. 316, 233-240, 1993

A;Reference number: S28989; PMID:93138130; PMID:8422949
A;Accession: S28989
A;Molecule type: protein
A;Residues: 1-27 <TER>
C;Superfamily: gamma-thionin

```

Query Match          47.2%; Score 142; DB 2; Length 27;
Best Local Similarity 96.0%; Pred. NO. 8.2e-09;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy

1 KLCERSSGTWSGVCNNACKNQCI 25
|||||

Dd

2 KLCEPSSGTWSGVCNNACKNQCI 26
|||||

RESULT 14

defensin AMP1 - *Clitoria ternatea*
 N/Alternate names: seed antifungal protein
 C/Species: *Clitoria ternatea*
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
 C/Accession: S66219
 R/Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven,
 FEBS Lett 368, 257-262, 1995
 A/Title: Isolation and Characterisation of plant defensins from seeds of Asteraceae, Fabae
 A/Reference number: S66218; MOID:95354848; PMID:7628617
 A/Accession: S66219
 A/Molecule type: protein
 A/Residues: 1-49 <OSB>
 C/Keywords: antifungal

Query Match	46.7%;	Score 140.5;	DB 2;	Length 49;
Best Local Similarity	49.1%;	Pred. No. 1.9e-08;		
Matches 26:	Conservative	5;	Mismatches 13;	Indels

QY 2 LCEBSSGTSWGCNNACNQICIRLEGAQHSC---NYVFFAHKCICYFPC 50
||||| : ||| ||| ||| : | : | : | :
Dh 2 TCFEASLTWTGCGNTGHDTOCRNWESAKHGACHKRGNW----KCFCYENC 49

RESULT 15

Reason: 13
 S28993
 antifungal protein 1 - white mustard (fragment)
 C:Species: Sinapis alba (white mustard)
 C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
 C:Accession: S28993
 R:Triras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, E.B.
 FEBS Lett. 315, 233-240, 1993
 A:Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
 A:Reference number: S28989; PMID:93138130; PMID:9422949
 A:Accession: S28993
 A:Molecule type: protein
 A:Residues: 1-25 <TER>
 C:Superfamily: gamma-thionin

Query Match 45.8%; Score 138; DB 2; Length 25;
Best Local Similarity 95.8%; Pred. No. 2.1e-08;
Matches 23; Conservative 0; Mismatches 1; Indels

Qy 1 KLCRSSGTWGSVCGNNACKNQ 24
|||
db 2 KLCRPSGTWGSVCGNNACKNQ 25

Search completed: May 11, 2004, 16:58:18
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:50:53 ; Search time 11 Seconds
(without alignments)
236.683 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCERSGTSWGVCGNNAC.....QHGSQNVFPAHKICICYPC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	301	100.0	79	1	AFP3_BRANA	Q39313 brassica na
2	301	100.0	79	1	AFP3_RAPSA	O24332 raphanus sa
3	282	93.7	80	1	AFP4_RAPSA	O24331 raphanus sa
4	281	93.4	80	1	AFP2_RAPSA	P30230 raphanus sa
5	279	92.7	51	1	AFPI_SINAL	P30231 sinapis alb
6	279	92.7	80	1	AFPI_BRANA	P30225 brassica na
7	279	92.7	80	1	AFPI_ARATH	O80995 arabidopsis
8	274	91.0	80	1	AFPI_ARATH	P30224 arabidopsis
9	273	90.7	51	1	AF2A_SINAL	P30232 sinapis alb
10	272	90.4	80	1	AFPI_ARATH	O80994 arabidopsis
11	272	90.4	80	1	AFPI_ARATH	Q9f123 arabidopsis
12	211.5	70.3	52	1	ASPI_SINAL	O10989 sinapis alb
13	145	48.2	161	1	ASPI_HELAN	P22357 helianthus
14	142	47.2	27	1	AFPI_BRARA	P30227 brassica ra
15	134	44.5	27	1	AFPI_BRARA	P30228 brassica ra
16	124	41.2	23	1	AFPI_BRANA	P30226 brassica na
17	90.5	30.1	75	1	DEFL_CAPAN	O43413 capsicum an
18	85.5	28.4	106	1	THGI_NICPA	O24115 nicotiana p
19	83.5	27.7	52	1	DEP2_SPIOL	P81571 spinacia ol
20	77.5	25.7	47	1	THGI_VAIZE	P81008 zea mays (m
21	75.5	25.1	47	1	THGI_WHEAT	P20158 triticum ae
22	75.5	25.1	105	1	THGF_TOBAC	P32026 nicotiana t
23	74.5	24.8	47	1	SA21_SORBI	Q03198 sorghum bic
24	74.5	24.8	47	1	SA13_SORBI	P21925 sorghum bic
25	74.5	24.8	47	1	THG_HORVU	P20230 hordeum vul
26	74	24.6	46	1	PSDI_PEA	P81929 pisum sativ
27	74	24.6	1408	1	SERE_DROME	P18168 drosophila
28	73	24.3	64	1	SCX2_LEIQH	P59355 leirurus qui
29	73	24.3	64	1	SCX3_BUTOC	P01485 buthus occi
30	73	24.3	85	1	SCX2_ANDAU	P01484 androctonus
31	73	24.3	85	1	SCXA_ANDAU	Q9blm4 androctonus
32	72.5	24.1	73	1	THG4_ARATH	Q9zul8 arabidopsis
33	71	23.6	46	1	AX2_ETVU	P82010 beta vulgar

34	70.5	23.4	47	1	PSD2_PEA	P81930 pisum sativ
35	70.5	23.4	72	1	D230_PEA	Q01783 pisum sativ
36	70.5	23.4	1394	1	LTBS_HUMAN	P22064 homo sapien
37	70.5	23.4	1595	1	LTBL_HUMAN	Q14766 homo sapien
38	70	23.3	74	1	DR39_PEA	Q01784 pisum sativ
39	69.5	23.1	47	1	THG2_WHEAT	P20159 triticum ae
40	69	22.9	65	1	SCXB_BUTOC	P01486 buthus occi
41	68	22.6	65	1	ITHC_HIRME	P28503 hirudo medi
42	68	22.6	670	1	S213_PAT	P46720 rattus norv
43	67	22.3	64	1	SCX5_LEIOU	P01481 leirurus qui
44	67	22.3	1213	1	JAG3_BRARE	Q90Y54 brachydanio
45	66.5	22.1	47	1	THGC_VIGUN	P83399 vigna ungu

ALIGNMENTS

RESULT 1

ID	APP3_BRANA	STANDARD;	PRT;	79 AA.
AC	Q39313;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cysteine-rich antifungal protein 3 precursor (AFP3).			
GN	AFP3.			
OS	Brassica napus (Rape).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids;			
OC	eurosids II; Brassicales; Brassicaceae; Brassica.			
OX	NCBI_TaxID=3708;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Naehan.			
RA	Sohn U., Lee C.M., Lee M.H., Kim J.H.;			
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: Possesses antifungal activity sensitive to inorganic			
CC	cations (By similarity).			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- SIMILARITY: Belongs to the plant defensin family.			

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CC	EMBL; U59459; AAB03224.1; -
DR	PIR; T07917; T07917.
DR	HSSP; P30231; 1AYJ.
DR	InterPro; IPR008176; Gamma-thionin.
DR	InterPro; IPR003614; Knot1.
DR	Fam; PF00304; Gamma-thionin; 1.
DR	ProDom; PD002594; G_Furothionin; 1.
DR	SMART; SM00505; Knot1; 1.
DR	PROSITE; PS00940; GAMMA_THIONIN; 1.
DR	Plant defense; Fungicide; signal; Multigene family.
FT	SIGNAL 1 29 POTENTIAL.
FT	CHAIN 30 79 CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
FT	DISULFID 32 79 BY SIMILARITY.
FT	DISULFID 43 64 BY SIMILARITY.
FT	DISULFID 49 73 BY SIMILARITY.
FT	DISULFID 53 75 BY SIMILARITY.
SQ	SEQUENCE 79 AA; 8555 MW; 3B5289FCFEA48936 CRC64;

Query Match 100.0%; Score 301; DB 1; Length 79;
 Best Local Similarity 100.0%; Pred. No. 5.4e-27;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACNQICIRLEGAGSCNYYFPAHKICICYPC 50

Db 30 KLCERSGTSWGVCGNNACKNQCIIRLEGAQHGSNCYVFFPAHKICICYFPC 79

RESULT 2

APP3_RAPSA STANDARD; PRT; 79 AA.
AC 024332;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 3 precursor (APP3).
GN APP3.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RL Submitter (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.

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EMBL; X97319; CAA65984.1; -;
PIR; T10243; T10243.
HSP; P30231; IAYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knott1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
SMART; SM00505; Knott1; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 79 CYS-THIONE-RICH ANTIFUNGAL PROTEIN 3.
FT MOD_RES 30 79 BY SIMILARITY.
FT DISULFID 32 79 BY SIMILARITY.
FT DISULFID 43 64 BY SIMILARITY.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 75 BY SIMILARITY.
FT SEQUENCE 79 AA; 8479 MW; BAF80465DB48548 CRC64;

Query Match 100.0%; Score 301; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.4e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQCIIRLEGAQHGSNCYVFFPAHKICICYFPC 50

Db 30 KLCERSGTSWGVCGNNACKNQCIIRLEGAQHGSNCYVFFPAHKICICYFPC 79

RESULT 3

APP4_RAPSA STANDARD; PRT; 80 AA.
AC 024331;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 4 precursor (APP4).
GN APP4.
OS Raphanus sativus (Radish).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
CC eurosid II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RL Submitter (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.

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EMBL; X97318; CAA65983.1; -;
PIR; T10183; T10183.
HSP; P30231; IAYJ.
InterPro; IPR008176; Gamma-thionin.
InterPro; IPR003614; Knott1.
Pfam; PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
SMART; SM00505; Knott1; 1.
PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Fungicide; Signal; Multigene family.
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 80 CYS-THIONE-RICH ANTIFUNGAL PROTEIN 4.
FT MOD_RES 30 80 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
FT SEQUENCE 80 AA; 8873 MW; B5F667B6441818C9 CRC64;

Query Match 93.7%; Score 282; DB 1; Length 80;
Best Local Similarity 90.0%; Pred. No. 6.9e-25;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQCIIRLEGAQHGSNCYVFFPAHKICICYFPC 50

Db 31 KLCERSGTSWGVCGNNACKNQCIIRLEGAQHGSNCYVFFPAHKICICYFPC 80

RESULT 4

APP2_RAPSA STANDARD; PRT; 80 AA.
AC P30230;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2 precursor (APP2).
GN APP2.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J.,

RA Cammue B.P.A., Broekaert W.F.;
 RT "Small cysteine-rich antifungal proteins from radish: their role in
 RL host defense.";
 RN Plant Cell 7:573-588(1995).
 RP [2]
 RC SEQUENCE OF 30-65.
 RX TISSUE=Seed;
 RA MEDLINE=92348373; PubMed=1639777;
 RA Terras F.R.G., Schoofs H.W.E., de Bolle M.F.C., van Leuven F.,
 RA Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "Analysis of two novel classes of plant antifungal proteins from
 RT radish (Raphanus sativus L.) seeds";
 RL J. Biol. Chem. 267:15301-15309(1992).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC -----
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 CC -----
 DR EMBL: U18556; AAA69540.1; -;
 DR PIR: T10823; T10823.
 DR HSP: P30231; IAYJ.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Knott1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G_Purothionin; 1.
 DR SMART: SM00505; Knott1; 1.
 DR PROSITE: PS00940; GAMMA-THIONIN; 1.
 DR Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 KN Pyrrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 30 CYSTEINE-RICH ANTIFUNGAL PROTEIN 2.
 FT MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 33 80 BY SIMILARITY.
 FT DISULFID 44 65 BY SIMILARITY.
 FT DISULFID 50 74 BY SIMILARITY.
 FT DISULFID 54 76 BY SIMILARITY.
 SQ SEQUENCE 80 AA; 8875 MW; 746110D9A8CE6370 CRC64;
 Query Match 93.48; Score 281; DB 1; Length 80;
 Best Local Similarity 92.0%; Pred. No. 8.9e-25;
 Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KLCRRSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 50
 Db 31 KLCRRSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 80
 RESULT 5
 AFPI_SINAL STANDARD; PRT; 51 AA.
 ID AFPI_SINAL
 AC P30231;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 (AFPI) (M1).
 OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;

RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RL antifungal proteins.";
 RN Int. J. Pept. Protein Res. 47:437-446(1996).
 RP [2]
 RC SEQUENCE OF 1-25.
 RX TISSUE=Seed;
 RA MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species";
 RL FEBS Lett. 316:233-240(1993).
 CC [3]
 CC STRUCTURE BY NMR.
 CC MEDLINE=9636715;
 CC Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
 RT "Determination of the three-dimensional solution structure of Raphanus
 RT sativus antifungal protein 1 by 1H NMR";
 RL J. Mol. Biol. 279:257-270(1998).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- MASS SPECTROMETRY: MW=5677; MW ERR=1.0; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC -----
 DR PDB: IAYJ; 28-JAN-98.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Knott1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G_Purothionin; 1.
 DR SMART: SM00505; Knott1; 1.
 DR PROSITE: PS00940; GAMMA-THIONIN; 1.
 DR Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.
 KW MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 4 51
 FT DISULFID 15 36
 FT DISULFID 21 45
 FT DISULFID 25 47
 FT STRAND 4 7
 FT HELIX 18 28
 FT STRAND 34 37
 FT STRAND 44 49
 SQ SEQUENCE 51 AA; 5695 MW; 770990E72DD1C469 CRC64;
 Query Match 92.7%; Score 279; DB 1; Length 51;
 Best Local Similarity 92.0%; Pred. No. 9.8e-25;
 Matches 46; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KLCRRSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 50
 Db 2 KLCRRSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 51
 RESULT 6
 AFPI_BRANA STANDARD; PRT; 80 AA.
 ID AFPI_BRANA
 AC P30225; Q41163;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 precursor (AFPI).
 GN AFPI.
 OS Brassica napus (Rape), and
 OS Raphanus sativus (Radish).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3709; 3726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=R.sativus; STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
 RX MEDLINE=95299350; PubMed=7780308;
 RA Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,

RA Kester A., Rees S.B., Torrekens S., Van Leuven F., Vanderleyden J.,
 RA Cammue B.P.A., Broekaert W.F.;
 RT "Small cysteine-rich antifungal proteins from radish: their role in
 RT host defense.";
 RL Plant Cell 7:568-573(1995).
 RN [2]
 RP SEQUENCE OF 30-73.
 RC SPECIES=B.napus; TISSUE=Seed;
 RX MEDLINE=93138130; Pubmed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 RN [3]
 RP SEQUENCE OF 30-73.
 RC SPECIES=R.sativus; TISSUE=Seed;
 RX MEDLINE=92348373; Pubmed=1639777;
 RA Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,
 RA Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "Analysis of two novel classes of plant antifungal proteins from
 RT radish (Raphanus sativus L.) seeds.";
 RL J. Biol. Chem. 267:15301-15309(1992).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U18557; AAA69541.1; -;
 DR PIR; T10176; T10176.
 DR HSSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knott1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 KW Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 80
 FT MOD RES 30 80
 FT CYS-STEINE-RICH ANTIFUNGAL PROTEIN 1.
 FT DISULFID 33 80
 FT BY SIMILARITY.
 FT DISULFID 44 65
 FT BY SIMILARITY.
 FT DISULFID 50 74
 FT BY SIMILARITY.
 FT DISULFID 54 76
 FT BY SIMILARITY.
 SQ SEQUENCE 80 AA; 8734 MW; 05B90FAAC8DA6C2B CRC64;
 Query Match 92.7%; Score 279; DB 1; Length 80;
 Best Local Similarity 92.0%; Pred. No. 1.5e-24;
 Matches 46; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KLCERSGTSWGVCGNNACKNQCILLEGAGHGSQNYVFAHKICICYFPC 50
 Db 31 KLCERPSGTWGVCGNNACKNQCINLEXARHGSQNYVFAHKICICYFPC 80

RESULT 7
 ID AF22_ARATH STANDARD; PRT; 80 AA.
 AC O80995;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Probable cysteine-rich antifungal protein At2g26010 precursor (APP).
 GN AT2G26010 OR T19118.18.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; Pubmed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Freus D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC
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 CC
 CC EMBL; AC004747; AAC31234.1; -;
 DR PIR; T02622; T02622.
 DR HSSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knott1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 KW Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 80
 FT MOD RES 30 30
 FT CYS-STEINE-RICH ANTIFUNGAL PROTEIN
 FT DISULFID 33 80
 FT BY SIMILARITY.
 FT DISULFID 44 65
 FT BY SIMILARITY.
 FT DISULFID 50 74
 FT BY SIMILARITY.
 FT DISULFID 54 76
 FT BY SIMILARITY.
 SQ SEQUENCE 80 AA; 8580 MW; 99E1E0D443AD67B CRC64;
 Query Match 92.7%; Score 279; DB 1; Length 80;
 Best Local Similarity 90.0%; Pred. No. 1.5e-24;
 Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KLCERSGTSWGVCGNNACKNQCILLEGAGHGSQNYVFAHKICICYFPC 50
 Db 31 KLCERPSGTWGVCGNNACKNQCINLEXARHGSQNYVFAHKICICYFPC 80

RESULT 8
 ID AF22_ARATH STANDARD; PRT; 80 AA.
 AC P30224; Q42179;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cysteine-rich antifungal protein 1 precursor (AFp1) (Anther-specific
DE protein S18 homolog).
GN AFp1 OR PF1.1 OR A1G75830 OR T4012.6 OR T4012.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Raynal M., Grelllet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Seed;
RA Raynal M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=99178804; PubMed=10080719;
RA Williams R.W., Clark S.E., Meyerowitz E.M.;
RL "Genetic and physical characterization of a region of Arabidopsis
chromosome 1 containing the CLAVATA1 gene.";
RL Plant Mol. Biol. 39:171-176(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
RL Nature 408:816-820(2000).
RN [5]
RP SEQUENCE OF 30-56.
RC TISSUE=Seed;
RX MEDLINE=93138130; PubMed=8422949;
RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
RT "A new family of basic cysteine-rich plant antifungal proteins from
Brassicaceae species.";
RL FEBS Lett. 316:233-240(1993).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
cations.
CC -!- SUBUNIT: Forms oligomers in its native state.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC -----
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CC -----
CC DE EMBL; Z27258; CAA81770.1; -.
CC EMBL; Z29957; CAA82845.1; -.

DR EMBL; X91916; CAA63009.1; -.
DR EMBL; AF049870; AAD02502.1; -.
DR EMBL; AC007396; AAF26754.1; -.
DR PIR; F96787; F96787.
DR HSSP; P30231; JAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00305; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
DR Plant defense; Fungicide; Signal; Multigene family;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29
FT CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
FT MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
FT CONFLICT 33 33 C -> F (IN REF. 1).
SQ SEQUENCE 80 AA; 8709 MW; 99F34A8DA360441F CRC64;
Query Match 91.0%; Score 274; DB 1; Length 80;
Best Local Similarity 90.0%; Pred. No. 5.3e-24;
Matches 45; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Oy 1 KLCERSGTWSGVCNNACKNQICRLGAQHGSQNYVFFPAHKICICYPC 50
Db 31 KLCERSGTWSGVCNNACKNQICRLGAQHGSQNYVFFPAHKICICYPC 80
RESULT 9
AF2A SIGNAL STANDARD; PRT; 51 AA.
AC P30232;
DC 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2A (AFP2A) (M2A).
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=96433791; PubMed=8836771;
RA Neumann G.M., Condron R., Polya G.M.;
RT "Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 kDa proteins. Identification as
antifungal proteins.";
RL Int. J. Pept. Protein Res. 47:437-446(1996).
RN [2]
RP SEQUENCE OF 1-26.
RC TISSUE=Seed;
RX MEDLINE=93138130; PubMed=8422949;
RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
RT "A new family of basic cysteine-rich plant antifungal proteins from
Brassicaceae species.";
RL FEBS Lett. 316:233-240(1993).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
cations.
CC -!- SUBUNIT: Forms oligomers in its native state.
CC -!- MASS SPECTROMETRY: MW=5705; MW_ERR=0.8; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the plant defensin family.
DR HSSP; P30231; JAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.

DR SMART; SM00505; Kntol; 1.
 DR PROSITE; PS00940; GAMMA-THIONIN; 1.
 KW Fungicide; Phosphorylation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 FT MOD_RES 15 15
 FT DISULFID 4 51
 FT DISULFID 15 36
 FT DISULFID 21 45
 FT DISULFID 25 47
 FT DISULFID 25 47
 SQ SEQUENCE 51 AA; 5722 MW; 1C7F50E72DC945B1 CRC64;

Query Match Score 273; DB 1; Length 51;
 Best Local Similarity 88.0%; Pred. No. 4.5e-24;
 Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLCRSSCTGWSGCGNNACNQCIRLEGQCHGSCNYYVPPAHKCIYFPC 50
 DB 2 KLCQPSGTGWSGCGNNACNQCINLEKARHGSCNYYVPPAHKCIYFPC 51

RESULT 10

APP3 ARATH
 ID APP3 ARATH STANDARD; PRT; 80 AA.
 AC O80394;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Probable cysteine-rich antifungal protein At2g26020 precursor (APP).
 GN AT2g26020 OR T19118.17.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman L.E., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.-J., Rensing C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768 (1999).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 cations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the plant defensin family.

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 CC

EMBL; AC004747; AAC31244.1; -.
 DR PIR; T02621; T02621.
 DR HSSP; P30231; LAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G. Purothionin; 1.
 DR SMART; SM00505; Kntol; 1.
 DR PROSITE; PS00940; GAMMA-THIONIN; 1.
 KW Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.

FT SIGNAL 1 29
 FT CHAIN 30 80
 FT MOD_RES 30 30
 FT DISULFID 33 80
 FT DISULFID 44 65
 FT DISULFID 50 74
 FT DISULFID 54 76
 SQ SEQUENCE 80 AA; 8640 MW; 81B106058BAFFCC7 CRC64;
 Query Match Score 272; DB 1; Length 80;
 Best Local Similarity 88.0%; Pred. No. 8.8e-24;
 Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLCRSSCTGWSGCGNNACNQCIRLEGQCHGSCNYYVPPAHKCIYFPC 50
 DB 31 KLCQPSGTGWSGCGNNACNQCINLEKARHGSCNYYVPPAHKCIYFPC 80

RESULT 11

APP4 ARATH
 ID APP4 ARATH STANDARD; PRT; 80 AA.
 AC Q9F123; P82786;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Probable cysteine-rich antifungal protein LCR77 precursor (APP).
 GN LCR77 OR AT5G44420 OR MFC16.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 P1 and TAC clones";
 RL DNA Res. 6:183-195 (1999).
 RN [2]
 RP IDENTIFICATION.
 RV Vanoosthuysen V., Miesge C., Dumas C., Cock J.M.;
 RL Submitted (JUN-2000) to Swiss-Prot.
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 cations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the plant defensin family.

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 CC

EMBL; AB017065; BAB09149.1; -.
 DR HSSP; P30231; LAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G. Purothionin; 1.
 DR SMART; SM00505; Kntol; 1.
 DR PROSITE; PS00940; GAMMA-THIONIN; 1.
 KW Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 80
 POTENTIAL.
 PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN

```

FT  MOD_RES      30  30  PYRROLIDONE CARBOXYLIC ACID (BY
FT  LCR77.
FT  SIMILARITY)
FT  33  80  BY SIMILARITY.
FT  44  65  BY SIMILARITY.
FT  50  74  BY SIMILARITY.
FT  54  76  BY SIMILARITY.
SQ  SEQUENCE  80 AA;  8518 MW;  2D0DAFB38E3B6321 CRC64;

Query Match      90.4%; Score 272; DB 1; Length 80;
Best Local Similarity 88.0%; Pred. No. 8.8e-24;
Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY  1 KLCERSSTGWSGVCGNNAKNCQIRLEGAGHGSNCNVVFFPAHKICIVFPC 50
DB  31 KLCERPSGTGWSGVCGNSACKNQCNINLEGAKHGSNCNVVFFPAHKICIVFPC 80

RESULT 12
AF2B SIGNAL
ID AF2B SIGNAL STANDARD; PRT; 52 AA.
AC Q10989;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2B (AFP2B) (M23).
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP TISSUE=Seed;
RC MEDLINE=96433791; PubMed=8836771;
RA Neumann G.M., Condron R., Polya G.M.;
RT "Purification and mass spectrometry-based sequencing of yellow
RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
RT antifungal proteins."
RL Int. J. Pept. Protein Res. 47:437-446(1996).
CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations.
CC -1- SUBUNIT: Forms oligomers in its native state.
CC -1- MASS SPECTROMETRY: MW=5840; MW ERR=1.2; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the plant defensin family.
DR HSP; P30231; IAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G-Purothionin; 1.
DR SMART; SM00505; Knto1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; FALSE NEG.
KW Fungicide; Pyrrolidone Carboxylic acid.
FT MOD_RES      4  1  PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
FT  DISULFID      4  52  BY SIMILARITY.
FT  DISULFID      16  37  BY SIMILARITY.
FT  DISULFID      22  46  BY SIMILARITY.
FT  DISULFID      26  48  BY SIMILARITY.
SQ  SEQUENCE  52 AA;  5856 MW;  A060FCBCL3A8D1PB CRC64;

Query Match      70.3%; Score 211.5; DB 1; Length 52;
Best Local Similarity 70.6%; Pred. No. 2.9e-17;
Matches 36; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY  1 KLCERSSTGWSGVCGNNAKNCQIRLEGAGHGSNCNVVFFPAHKICIVFPC 50
DB  2 KLCARPSGTGWSGVCGNNAKNCQIRLEGAGHGSNCNVVFFPAHKICIVFPC 52

RESULT 13
ASFI_HELAN
ID ASFI_HELAN STANDARD; PRT; 161 AA.
AC P22357;

QY  1 KLCERSSTGWSGVCGNNAKNCQIRLEGAGHGSNCNVVFFPAHKICIVFPC 50
DB  16 KICEKPSKTWFGNCKDTCDCRCIDWEGAKHGACHQREAKHMCFCYFDC 65

Query Match      48.2%; Score 145; DB 1; Length 161;
Best Local Similarity 46.0%; Pred. No. 1.9e-09;
Matches 23; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY  1 KLCERSSTGWSGVCGNNAKNCQIRLEGAGHGSNCNVVFFPAHKICIVFPC 50
DB  16 KICEKPSKTWFGNCKDTCDCRCIDWEGAKHGACHQREAKHMCFCYFDC 65

RESULT 14
AFPI_BRARA
ID AFPI_BRARA STANDARD; PRT; 27 AA.
AC P30227;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 1 (AFPI) (Fragment).
OS Brassica rapa (Turnip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Anther-specific protein SF18 precursor (Fragment).
OS Helianthus annuus (Common sunflower)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. HA401B / Cargill; TISSUE=Anther;
RX MEDLINE=9138702; PubMed=2102380;
RT Domon C., Eyraud J.-L., Herdenger F., Pillay D.T.N., Steinmetz A.;
RT "Nucleotide sequence of two anther-specific cDNAs from sunflower
RT (Helianthus annuus L.).";
RL Plant Mol. Biol. 15:643-646(1990).
CC -1- FUNCTION: Anther-specific cell wall protein which could contribute
CC to the cell wall architecture of epidermal anther cells via
CC intermolecular disulfide bridges.
CC -1- TISSUE SPECIFICITY: Epidermal anther cells.
CC -1- DEVELOPMENTAL STAGE: Late developmental stages.
CC -1- SIMILARITY: Belongs to the plant defensin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X53375; CAA37455.1; -
DR PIR; S12246; S12246.
DR HSP; P30231; IAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G-Purothionin; 1.
DR SMART; SM00505; Knto1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Signal; Cell wall.
FT NON_TER      1  1
FT SIGNAL        1  8
FT CHAIN         9  161 ANTH-ER-SPECIFIC PROTEIN SF18.
FT DOMAIN        9  65 GAMMA-THIONIN LIKE DOMAIN.
FT DOMAIN       70  161 PROLINE DOMAIN.
FT DISULFID      18  65 BY SIMILARITY.
FT DISULFID      29  50 BY SIMILARITY.
FT DISULFID      35  59 BY SIMILARITY.
FT DISULFID      39  61 BY SIMILARITY.
SQ  SEQUENCE  161 AA;  15363 MW;  27A9CF4633ADA02B CRC64;

Query Match      48.2%; Score 145; DB 1; Length 161;
Best Local Similarity 46.0%; Pred. No. 1.9e-09;
Matches 23; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY  1 KLCERSSTGWSGVCGNNAKNCQIRLEGAGHGSNCNVVFFPAHKICIVFPC 50
DB  16 KICEKPSKTWFGNCKDTCDCRCIDWEGAKHGACHQREAKHMCFCYFDC 65

RESULT 14
AFPI_BRARA
ID AFPI_BRARA STANDARD; PRT; 27 AA.
AC P30227;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 1 (AFPI) (Fragment).
OS Brassica rapa (Turnip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=51350;
 RN [1]
 RC SEQUENCE.
 RP TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species."
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR FIR; S28989; S28989.
 DR HSSP; P30231; 1AYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF003104; Gamma-thionin; 1.
 DR ProDom; PD002594; G_Purothionin; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2925 MW; 4C85BD9C611D4A9E CRC64;

Query Match 47.2%; Score 142; D3 1; Length 27;
 Best Local Similarity 96.0%; Pred.No.7.6e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLCERSGTWSGVCNNACKNQC1 25
 |||||
 DB 2 KLCERPSGTWSGVCNNACKNQC1 26

RESULT 15

AF2_BRARA
 ID APP2_BRARA STANDARD; PRT; 27 AA.
 AC P30228;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2 (APP2) (Fragment).
 OS Brassica rapa (turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=51350;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species."
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses some antifungal activity sensitive to
 CC inorganic cations and antibacterial activity against B.megaterium.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR FIR; S28990; S28990.
 DR HSSP; P30231; 1AYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR ProDom; PD002594; G_Purothionin; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Antibiotic; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT UNSURE 27 27
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;

Query Match 44.5%; Score 134; DB 1; Length 27;
 Best Local Similarity 92.3%; Pred.No.5.8e-09;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KLCERSGTWSGVCNNACKNQC1 26
 |||||
 DB 2 KLCERPSGTWSGVCNNACKNQC1 27

Search completed: May 11, 2004, 16:57:18
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:53:44 ; Search time 39 Seconds
(without alignments)
404.511 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCERSSGTWSGCGNNAC.....QHGSNNYVPAHKICICYFPC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	94.4	80	10 Q94IN7	Q94IN7 brassica ol
2	283	94.0	80	10 Q8H6K0	Q8H6K0 brassica ra
3	279	92.7	80	10 Q9FS38	Q9FS38 eutrema was
4	272	90.4	80	10 Q9FI22	Q9FI22 arabidopsis
5	167	55.5	56	10 Q9FWR6	Q9FWR6 arabidopsis
6	167	55.5	78	10 Q8VZQ7	Q8VZQ7 arabidopsis
7	154	51.2	108	10 Q8LSM8	Q8LSM8 helianthus
8	129	42.9	132	10 Q84ZX5	Q84ZX5 artemisia v
9	116.5	38.7	80	10 Q9FZ31	Q9FZ31 arabidopsis
10	116.5	38.7	83	10 Q40779	Q40779 picea abies
11	115.5	38.4	83	10 Q8GTL2	Q8GTL2 picea abies
12	101.5	33.7	83	10 Q40539	Q40539 nicotiana t
13	86.5	28.7	77	10 P82788	P82788 arabidopsis
14	83.5	27.7	108	10 P82789	P82789 arabidopsis
15	82.5	27.4	105	10 Q40128	Q40128 lycopersico
16	81.5	27.1	81	10 Q948T2	Q948T2 pyrus pyrif

17	81.5	27.1	87	10 Q948T3	Q948T3 pyrus pyrif
18	81.5	27.1	87	10 Q948T4	Q948T4 pyrus pyrif
19	81.5	27.1	105	10 Q24105	Q24105 nicotiana e
20	81.5	27.1	559	5 Q9VZ44	Q9VZ44 drosophila
21	80.5	26.7	55	10 Q9C947	Q9C947 arabidopsis
22	80.5	26.7	76	10 Q8LEG6	Q8LEG6 arabidopsis
23	77.5	25.7	105	10 Q8GTMO	Q8GTMO nicotiana a
24	76.5	25.4	78	10 Q8W4V6	Q8W4V6 capsicum an
25	76.5	25.4	382	11 Q8K1E3	Q8K1E3 mus musculu
26	75.5	25.1	101	10 Q8H6Q0	Q8H6Q0 petunia hyb
27	75.5	25.1	794	5 Q8T4P0	Q8T4P0 lytechinus
28	75	24.9	85	5 Q7YXD3	Q7YXD3 androctonus
29	74.5	24.8	49	10 Q93WS9	Q93WS9 musa acumin
30	74	24.6	950	5 Q8MQN5	Q8MQN5 drosophila
31	74	24.6	1404	5 Q9VB65	Q9VB65 drosophila
32	73.5	24.4	684	5 Q81498	Q81498 cupressus
33	73.5	24.4	2233	5 Q94711	Q94711 paramacium
34	73	24.3	107	10 Q9XHE3	Q9XHE3 capsicum ch
35	72.5	24.1	129	10 Q8L8U0	Q8L8U0 arabidopsis
36	72.5	24.1	129	10 P82773	P82773 arabidopsis
37	72	23.9	721	13 Q7ZT69	Q7ZT69 lampetra ja
38	71.5	23.8	77	10 Q8H766	Q8H766 elaeis guin
39	71.5	23.8	78	10 Q8WB66	Q8WB66 nicotiana t
40	71.5	23.8	81	10 Q24225	Q24225 oryza sativ
41	70.5	23.4	72	10 Q9FR81	Q9FR81 pisum sativ
42	70.5	23.4	75	10 Q8W434	Q8W434 vigna radia
43	70.5	23.4	77	10 Q8LGD4	Q8LGD4 arabidopsis
44	70.5	23.4	78	10 Q8S8H3	Q8S8H3 arabidopsis
45	70.5	23.4	82	10 Q8L698	Q8L698 triticum ae

ALIGNMENTS

RESULT 1

Q94IN7 ID Q94IN7 PRELIMINARY; PRT; 80 AA.

AC Q94IN7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Defensin precursor.
GN DEF.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA Benault R.;
RT "Brassica oleracea def gene for defensin.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AJ311046; CAC37558.1;
DR GO: GO:0003793, P:defense/immunity protein activity; IEA.
DR InterPro: IPR008176; Gamma-thionin.
DR InterPro: IPR003614; Knott.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR SMART: SM00505; KncE1; 1.
DR PROSITE: PS00940; GAMMA_THIONIN; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 80 AA; 8740 MW; 980477DFBD8D2690 CRC64;
1 29 POTENTIAL.

Query Match 94.4%; Score 284; DB 10; Length 80;

Best Local Similarity 94.0%; Pred. No. 1e-29; Mismatches 1; Gaps 0;

Matches 47; Conservative 1; Indels 0;

Qy 1 KLCERSSGTWSGCGNNACKQCIRLEGAHQHSCNYYVPAHKICICYFPC 50

Db 31 KLCERSSGTWSGCGNNACKQCIRLEGAHQHSCNYYVPAHKICICYFPC 80

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RESULT 2
Q8H6K0 Q8H6K0 PRELIMINARY; PRT; 80 AA.
AC Q8H6K0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Defense.
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP SEQUENCE FROM N.A.
RA Ryang S.-H., Chung S.-Y., Park Y.-S., Cho T.-J.;
RT "Characterization of Chinese cabbage genes induced by Pseudomonas
   syringae pv. tomato".
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528180; AAN23105.1; -.
GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SMO0505; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
SQ SEQUENCE 80 AA; 8864 MW; 485CCSA9505E92C CRC64;

Query Match 94.0%; Score 283; DB 10; Length 80;
Best Local Similarity 92.0%; Pred. No. 1.4e-29;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCERSSGTWSGCGNNACKNQCIRLEGAGHSGSNYPVPAHKICYPFC 50
Db 31 KLCERSSGTWSGCGNNACKNQCINLEGARHGSCNYPVPHRCICYPFC 80

RESULT 3
Q9FS38 Q9FS38 PRELIMINARY; PRT; 80 AA.
AC Q9FS38;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Gamma-thionin precursor.
OS Eutrema wasabi.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Eutrema.
OX NCBI_TaxID=75806;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Leaf, and Stem;
RX MEDLINE=21071227; PubMed=11204773;
RA Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
RT "Production of antimicrobial defensin in Nicotiana benthamiana with a
   potato virus X vector".
RL Mol. Plant Microbe Interact. 14:111-115 (2001).
DR EMBL; AB012871; BAB19054.1; -.
DR HSSP; P30231; IAYJ.
GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SMO0505; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW SIGNAL.
FT CHAIN 1 29 POTENTIAL.
FT CHAIN 30 80 POTENTIAL.
SQ SEQUENCE 80 AA; 8761 MW; CF2F10ADD38FC87A CRC64;

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Query Match 92.7%; Score 279; DB 10; Length 80;
Best Local Similarity 88.0%; Pred. No. 4.6e-29;
Matches 44; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCERSSGTWSGCGNNACKNQCIRLEGAGHSGSNYPVPAHKICYPFC 50
Db 31 KLCERSSGTWSGCGNNACKNQCINLEGARHGSCNYPVPHRCICYPFC 80

RESULT 4
Q9FI22 Q9FI22 PRELIMINARY; PRT; 80 AA.
AC Q9FI22;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Antifungal protein-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Columbia;
RX MEDLINE=99397451; PubMed=10470850;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
   Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
   Sequence features of the regions of 1,011,550 bp covered by seventeen
   P1 and TAC clones."
RL DNA Res. 6:183-195 (1999).
DR EMBL; AB017065; BAB09150.1; -.
DR HSSP; P30231; IAYJ.
GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SMO0505; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
SQ SEQUENCE 80 AA; 8550 MW; 44E1F6D8452AC76E CRC64;

Query Match 90.4%; Score 272; DB 10; Length 80;
Best Local Similarity 88.0%; Pred. No. 3.9e-28;
Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLCERSSGTWSGCGNNACKNQCIRLEGAGHSGSNYPVPAHKICYPFC 50
Db 31 KLCERSSGTWSGCGNNACKNQCINLEGARHGSCNYPVPAHKICYPFC 80

RESULT 5
Q9FWR6 Q9FWR6 PRELIMINARY; PRT; 56 AA.
AC Q9FWR6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE F14P1.6 protein.
RN F14P1.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.P.,
   Altati H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
   Buehler E., Chao Q., Chin C., Chioi J., Choi E., Gonzalez A.,
   Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,

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RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
 RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024609; AAF98402.1; -;
 DR PIR: G86328; G86328.
 DR HSPF: F30231; IAU.
 DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro: IPR008176; Gamma-thionin.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G Purothionin; 1.
 DR SMART: SM00505; Knt1; 1.
 DR PROSITE: PS00940; GAMMA THIONIN; 1.
 SQ SEQUENCE 56 AA; 6403 MW; 3BD56EAA25EBC442 CRC64;
 Query Match 55.5%; Score 167; DB 10; Length 56;
 Best Local Similarity 52.0%; Pred. No. 1.6e-14;
 Matches 26; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
 QY 1 KLCRRSGTWSGVCNNACKNQCIRLEGAGHSCNYPFAHKCIYFPC 50
 Db 7 RICERRSKTWTGFCNTRGCDSCQCKRWERASHGACHAQFPFGACFCYFNC 56
 RESULT 6
 QVZQ7 PRELIMINARY; PRT; 78 AA.
 AC QVZQ7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative defensin APL1 protein.
 GN At1g19610.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Ban J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
 RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL "Full length cDNA of gene At1g19610 (GI:15223595).";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Ban J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Tang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL "Arabidopsis Open Reading Frame (ORF) Clones";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY063933; AAL36289.1; -;
 DR EMBL: AY114038; AAW45086.1; -;
 DR InterPro: IPR008176; Gamma-thionin.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G Purothionin; 1.
 DR PROSITE: PS00940; GAMMA THIONIN; 1.
 SQ SEQUENCE 78 AA; 8840 MW; A5B5DD28303A6545 CRC64;
 Query Match 55.5%; Score 167; DB 10; Length 78;
 Best Local Similarity 52.0%; Pred. No. 2.2e-14;
 Matches 26; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 KLCRRSGTWSGVCNNACKNQCIRLEGAGHSCNYPFAHKCIYFPC 50
 Db 29 RICERRSKTWTGFCNTRGCDSCQCKRWERASHGACHAQFPFGACFCYFNC 78
 RESULT 7
 QVZQ7 PRELIMINARY; PRT; 108 AA.
 AC QVZQ7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Defensin.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Heliantheae;
 OC Helianthus.
 OC NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hu X., Bidney D., Duvick J., Yalpani N., Crasta O., Folkerts O.,
 RA Lu G.;
 RL "Oxalate oxidase confers Sclerotinia resistance.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF364865; AAM27914.1; -;
 DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Knt1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G Purothionin; 1.
 DR SMART: SM00505; Knt1; 1.
 SQ SEQUENCE 108 AA; 11866 MW; 631ECD8F02F21AD0 CRC64;
 Query Match 51.2%; Score 154; DB 10; Length 108;
 Best Local Similarity 50.0%; Pred. No. 1.5e-12;
 Matches 25; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
 QY 1 KLCRRSGTWSGVCNNACKNQCIRLEGAGHSCNYPFAHKCIYFPC 50
 Db 29 ELCEKASQTWSGTCGKTKHCDCKSWEGAHGACHVDRGKEMCFYFNC 78
 RESULT 8
 QVZQ7 PRELIMINARY; PRT; 132 AA.
 AC QVZQ7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Major pollen allergen Art v 1 precursor.
 OS Artemisia vulgaris (Mugwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Anthemideae;
 OC Artemisia.
 OC NCBI_TaxID=4220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen;
 RX MEDLINE=22409970; PubMed=12475905;
 RA Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N.,
 RA Altmann F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.;
 RL "Art v 1, the major allergen of mugwort pollen, is a modular
 glycoprotein with a defensin-like and a hydroxyproline-rich domain.";
 RL FASEB J. 17:106-108(2003).
 DR EMBL: AF493943; AAC24900.1; -;
 DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Knt1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR SMART: SM00505; Knt1; 1.

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Query Match      38.7%; Score 116.5; DB 10; Length 80;
Best Local Similarity 39.2%; Pred. No. 9.6e-08;
Matches 20; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

QY 1 KLCRSSGTWSGVCNNACKNOCIRLEGAHQGSCNYVPPAHKCICYPPC 50
   :||:|||||:||||:||||:||||:||||:||||:||||:||||:
DB 30 ELCKRETSWGRKCVNDYQCRDHCINNDRGNDGYCAGGYPWYRSCFCFFSC 80
   :||:|||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 10
Q40779 PRELIMINARY; PRT; 83 AA.
AC Q40779;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative gamma-thionin protein precursor.
SP11.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Sharma P., Linneborg A.;
RT "Isolation and characterization of a cDNA encoding a gamma-thionin-
RT like protein from roots of Norway spruce.";
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X91487; CAA62761.1; -.
DR PIR; T14866; T14866.
DR HSSP; P41964; IMYN.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 32 POTENTIAL
SEQUENCE 83 AA; 8835 MW; B94207ADAB8FE4A5 CRC64;

Query Match      38.7%; Score 116.5; DB 10; Length 83;
Best Local Similarity 42.0%; Pred. No. 9.9e-08;
Matches 21; Conservative 8; Mismatches 20; Indels 1; Gaps 1;

QY 1 KLCRSSGTWSGVCNNACKNOCIRLEGAHQGSCNYVPPAHKCICYPPC 50
   :||:|||||:||||:||||:||||:||||:||||:||||:||||:
DB 34 RTCKTPSGKFGVCASSNCKNVC-QTEGPPSGSCDFHVANKKCYCSKPC 82
   :||:|||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
Q8GT12 PRELIMINARY; PRT; 83 AA.
AC Q8GT12;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative plant defensin SP11B.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Needle;
RA Fossdal C.G.;
RT "The putative gymnosperm plant defensin (SP11) accumulates after seed
RT germination and a related SP11B cDNA is found in needles.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548021; AAN40688.1; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.

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DR InterPro: IPR008176; Gamma-thionin.
DR InterPro: IPR003614; Knot1.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR SMART: SM00505; Knot1; 1.
DR PROSITE: PS00940; GAMMA THIONIN; 1.
SQ SEQUENCE 83 AA; 8888 MW; E45BF9561B9AA3D2 CRC64;

Query Match 38.4%; Score 115.5; DB 10; Length 83;
Best Local Similarity 42.0%; Pred. No. 1.3e-07;
Matches 21; Conservative 7; Mismatches 21; Indels 1; Gaps 1;

Qy 1 KLCERSGTVSGVCGNNACKQCIRLEGAGHGSNCNVFPAHKICICYFPC 50
Dy 34 RTCKTPSGKFGVCASRNCKNVC-QTEGFPSCDFHVANRKCVCSEK 82

RESULT 12
Q40539 PRELIMINARY; PRT; 83 AA.
AC Q40539;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pti1 protein.
GN Pti1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Samsung;
RC InterPro: IPR008176; Gamma-thionin.
RA "Cloning and sequencing of the cDNAs induced by aluminium treatment and Pi starvation in cultured tobacco cells.";
RL Physiol. Plantarum 93:11-18(1995).
DR EMBL: D29679; BAA06149.1; -.
DR PIR: TC3673; T03673.
DR HSP: P30231; IAYJ.
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR SMART: SM00505; Knot1; 1.
DR PROSITE: PS00940; GAMMA THIONIN; 1.
SQ SEQUENCE 83 AA; 9700 MW; 64780A4984E371B0 CRC64;

Query Match 33.7%; Score 101.5; DB 10; Length 83;
Best Local Similarity 40.4%; Pred. No. 9.2e-06;
Matches 21; Conservative 6; Mismatches 22; Indels 3; Gaps 2;

Qy 1 KLCERSGTVSGVCGNNACKQCIRLEGAGHGSNCNVFPAHKICICYFPC 50
Dy 32 KLCRRKSTPSGYCFISEHCECKEKGAGRGVCKISIFRRY-CYCYHKC 82

RESULT 13
P82788 PRELIMINARY; PRT; 77 AA.
ID P82788
AC P82788;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein LCR79 precursor.
GN LCR79.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

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RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Barnstead M.E., Feldblum T.V.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Bowning C.M., Koo H., Moffat K.S.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon L.J., Gill J.E.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L.,
RA Adams M.B., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana";
RL Nature 402:761-768(1999).
RN SEQUENCE FROM N.A.
RP IDENTIFICATION.
RC PubMed=11437247;
RA Vancosthuyse V., Miesge C., Dumas C., Cock J.M.;
RA "Two large Arabidopsis thaliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the male component of the self-incompatibility response.";
RL Plant Mol. Biol. 46:17-34(2001).
CC -!- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.
DR EMBL: AC006223; -; NOT ANNOTATED CDS.
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR PROSITE: PS00940; GAMMA THIONIN; FALSE NEG.
KW Hypothetical protein; Signal; Plant defense.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 77 HYPOTHETICAL PROTEIN LCR79.
FT DISULFID 28 72 BY SIMILARITY.
FT DISULFID 39 59 BY SIMILARITY.
FT DISULFID 45 66 BY SIMILARITY.
FT DISULFID 49 68 BY SIMILARITY.
SQ SEQUENCE 77 AA; 8909 MW; 97194D61E5620DBE CRC64;

Query Match 28.7%; Score 86.5; DB 10; Length 77;
Best Local Similarity 38.0%; Pred. No. 0.0008;
Matches 19; Conservative 4; Mismatches 24; Indels 3; Gaps 2;

Qy 1 KLCERSGTVSGVCGNNACKQCIRLEGAGHGSNCNVFPAHKICICYFPC 50
Dy 26 QMCEAKSLDWKMLKWRNCRQVCIS-EGFTDGRCKGF--TRKICICKRPC 72

RESULT 14
P82789 PRELIMINARY; PRT; 108 AA.
ID P82789
AC P82789;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein LCR80 precursor.
GN LCR80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asanizu E., Miyajima N.,
RA Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,361,565 bp covered by twenty one physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
RN IDENTIFICATION.
RP PubMed=11437247;

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RA Vanoosthuyse V., Miesse C., Dumas C., Cock J.M.;
RT "Two large Arabidopsis thaliana gene families are homologous to the
RT Brassica gene superfamily that encodes pollen coat proteins and the
RT male component of the self-incompatibility response.";
RL Plant Mol. Biol. 46:17-34(2001).
DR EMBL: AB011481; -; NOT ANNOTATED CDS.
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003614; Knot1.
DR SMART; SM00505; Knot1; 1.
DR Hypothetical protein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 108 HYPOTHETICAL PROTEIN LCR80.
SQ SEQUENCE 108 AA; 11551 MW; 11E28E2CCE3578A7 CRC64;

Query Match 27.7%; Score 83.5; DB 10; Length 108;
Best Local Similarity 32.0%; Pred. No. 0.0027;
Matches 16; Conservative 4; Mismatches 29; Indels 1; Gaps 1;

Qy 1 KLCERSGTSWGVCGNNACKNCICIRLEGAQHGSNCNYVPPAHKICICYPPC 50
Db 60 KLCNGGLGCGESC-NEQCDCRNCQRYNGHGYCNTLDDFSLCLCKYPC 108

RESULT 15
Q00128 PRELIMINARY; PRT; 105 AA.
AC Q00128;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Flower-specific gamma-thionin-like protein/acidic protein
DE precursor.
DE Lycopodium esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF36; TISSUE=Pistil;
RX MEDLINE=95375233; PubMed=7647301;
RA Milligan S.B., Gasser C.S.;
RT "Nature and regulation of pistil-expressed genes in tomato.";
RL Plant Mol. Biol. 28:691-711(1995).
DR EMBL: U20591; AAA80496.1; -.
DR PIR: S57809;
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD02594; G Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 73 GAMMA-THIONIN-LIKE PROTEIN.
FT CHAIN 74 105 ACIDIC PROTEIN.
SQ SEQUENCE 105 AA; 11914 MW; ADC9B7ECB620E814 CRC64;

Query Match 27.4%; Score 82.5; DB 10; Length 105;
Best Local Similarity 32.0%; Pred. No. 0.0036;
Matches 16; Conservative 13; Mismatches 18; Indels 3; Gaps 2;

Qy 1 KLCERSGTSWGVCGNNACKNCICIRLEGAQHGSNCNYVPPAHKICICYPPC 50
Db 27 QICKAPSQTPPLGLCFMDSSCKYCIK-EXFTGHCCKL--QRKCLCTKPC 73

Search completed: May 11, 2004, 16:57:46
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 10:11:08 ; Search time 1734 Seconds
(without alignments)
1249.799 Million cell updates/sec

Title: US-10-006-252a-10
Perfect score: 301
Sequence: 1 KLCRRSSGTSWGVGNAC.....QHGSNCYVPAHKICICYPC 50

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -NORM=ext -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=US10006252 @CGN_1.1.5265 @runat_11052004_141947_10947 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCKS=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: gb.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*

- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	301	100.0	451	8	BNUS9459
2	301	100.0	475	8	RSEFP3
3	284	94.4	933	8	BOL311046
4	283	94.0	363	8	AF528180
5	282	93.7	499	8	RGAFF4
6	281	93.4	285	6	AR014693
7	281	93.4	285	6	AR432393
8	281	93.4	288	6	AR5553
9	281	93.4	288	6	AR050161
10	281	93.4	288	6	AR130280
11	281	93.4	288	6	I23736
12	281	93.4	308	6	AR014682
13	281	93.4	308	6	AR432382
14	281	93.4	449	6	E34290
15	281	93.4	457	8	RSU18556
16	281	93.4	522	6	BD223233
17	281	93.4	534	6	BD240936
18	281	93.4	534	6	BD223234
19	281	93.4	534	6	BD223237
20	281	93.4	606	6	BD223236
21	279	92.7	243	6	BD174927
22	279	92.7	285	6	AR014692
23	279	92.7	285	6	AR432392
24	279	92.7	395	8	RSU18557
25	279	92.7	414	6	A26875
26	279	92.7	414	6	A39549
27	279	92.7	414	6	A63404
28	279	92.7	414	6	AR050153
29	279	92.7	414	6	AR130272
30	279	92.7	414	6	E31545
31	279	92.7	414	6	I23728
32	279	92.7	414	6	AR207337
33	279	92.7	414	6	AR374914
34	279	92.7	414	8	AB012871
35	279	92.7	497	11	BV010712
36	279	92.7	541	11	BV010697
37	279	92.7	87080	8	AC004747
38	274	91.0	243	6	AX412406
39	274	91.0	243	6	AX412601
40	274	91.0	243	6	AX651878
41	274	91.0	243	6	BD174928
42	274	91.0	243	8	AY060506
43	274	91.0	403	6	A68645
44	274	91.0	403	8	AYANTSPEC
45	274	91.0	416	6	E31546

BN59459 451 bp mRNA linear PLN 29-JUN-1996
 LOCUS Brassica napus antifungal protein mRNA, complete cds.
 DEFINITION U59459 H07366
 ACCESSION U59459.1 GI:1399229
 VERSION
 KEYWORDS
 SOURCE Brassica napus (rape)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 451)
 AUTHORS Sohn,U., Lee,C.M., Lee,M.H. and Kim,J.H.
 TITLE Brassica napus CDNA
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 451)
 AUTHORS Sohn,U., Lee,C.M., Lee,M.H. and Kim,J.H.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-1996) Department of Genetic Engineering, Kyungpook National University, Puk-Ku, Sankyuk-Dong 1370, Taegu 702-701, Korea
 COMMENT On Jul 1, 1996 this sequence version replaced gi:12933377.
 FEATURES
 source
 1. .451
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Naehan"
 /db_xref="taxon:3708"
 /note="transcript putatively induced by Scroerotinia scroerotiium in infected Brassica napus"
 26. .265
 CDS
 /codon_start=1
 /product="antifungal protein"
 /protein_id="AA503224.1"
 /db_xref="GI:1399230"
 /translation="MAKFAIITLLPAAIVFAFAEPTVMVEAKLCERSSGTWSGVCG
 NNNACKNQICIRLEGAHQSCNVYFPAHKICVYFC"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.04e-29 Length: 451
 Score: 301.00 Matches: 50
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-10-006-252A-10 (1-50) x BN59459 (1-451)
 QY 1 LysLeuCySGluArgSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 113 AAGTTGTGCGAGAGTCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGCTGC 172
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTy-ValPhePro 40
 Db 173 AAGAATCAGTGCATTCGACTTGAAGGAGCACAACTGATCATGCAACTATGTGTTCCCT 232
 QY 41 AlaHisLysCysIleCysTyPheProCys 50
 Db 233 GCTCACAAGTGTATCTGTTATTTCCCATGT 262
 RESULT 2
 RSEFP3
 LOCUS R.sativus mRNA for antifungal protein 3.
 DEFINITION X97319
 ACCESSION X97319.1 GI:1655684
 VERSION
 KEYWORDS AFP; antifungal protein 3.
 SOURCE Raphanus sativus (radish)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

1 Terras,F.R.G., Goderis,I.J., Penninckx,I.J., Osborn,R.W. and
 Broekaert,W.F.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 475)
 AUTHORS Terras,F.R.G.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-1996) F.R.G. Terras, Institut fur pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg 3, Halle (Saale), D-06120, FRG
 FEATURES
 source
 1. .475
 Location/Qualifiers
 /organism="Raphanus sativus"
 /mol_type="mRNA"
 /cultivar="Ronde Rode Kleine Witpunt"
 /db_xref="taxon:3726"
 /dev_stage="adult plants infected with Alternaria brassicicola"
 1. .475
 /gene="AFP"
 28. .267
 /gene="AFP"
 /codon_start=1
 /product="antifungal protein 3"
 /protein_id="CAA6584.1"
 /db_xref="GI:1655685"
 /db_xref="GOA:O24332"
 /db_xref="SWISS-PROT:O24332"
 /translation="NAKFAIIVALLPAAIVFAFAEPTVMVEAKLCERSSGTWSGVCG
 NNNACKNQICIRLEGAHQSCNVYFPAHKICVYFC"
 28. .114
 sig_peptide
 115. .264
 mat_peptide
 /gene="AFP"
 /product="antifungal protein 3"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.11e-29 Length: 475
 Score: 301.00 Matches: 50
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-10-006-252A-10 (1-50) x RSEFP3 (1-475)
 QY 1 LysLeuCySGluArgSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 115 AAGTTGTGCGAGAGTCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACGATGC 174
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTy-ValPhePro 40
 Db 175 AAGAATCAGTGCATTCGACTTGAAGGAGCACAACTGATCATGCAACTATGTGTTCCCT 234
 QY 41 AlaHisLysCysIleCysTyPheProCys 50
 Db 235 GCTCACAAGTGTATCTGTTATTTCCCATGT 264
 RESULT 3
 BOL311046
 LOCUS Brassica oleracea def gene for defensin.
 DEFINITION AJ311046
 ACCESSION AJ311046.1 GI:13872713
 VERSION
 KEYWORDS def gene; defensin.
 SOURCE Brassica oleracea
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1
 AUTHORS Esnault,R.

DEFINITION	Brassica rapa subsp. pekinensis defensin mRNA, complete cds.
ACCESSION	AF528180
VERSION	AF528180.1 GI:23321204
KEYWORDS	
SOURCE	Brassica rapa subsp. pekinensis
ORGANISM	Brassica rapa subsp. pekinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE	1 (bases 1 to 363) Ryang,S.-H., Chung,S.-Y., Park,Y.-S. and Cho,T.-J. Characterization of Chinese cabbage genes induced by Pseudomonas syringae pv. tomato
AUTHORS	Unpublished
TITLE	2 (bases 1 to 363) Park,Y.-S., Chung,S.-Y. and Cho,T.-J.
JOURNAL	Direct Submission Submitted (10-JUL-2002) Division of Life Sciences, Chungbuk National University, Gae-Shin-Dong San 48, Cheongju 360-763, Korea
FEATURES	Location/Qualifiers 1..363 /organism="Brassica rapa subsp. pekinensis" /mol_type="mRNA" /sub_species="pekinensis" /db_xref="taxon:51351" 22..264 /note="induced by Pseudomonas syringae pv. tomato" /codon_start=1 /product="defensin" /protein_id="AAN23105.1" /db_xref="GI:23321205" /translation="MAKFSVITLTFEALVLFAFEAPTVMKAKLCERSSGTWSGVC GNNACKQCCINLEGARHGSCNIVFPARHCICYPFC"
CDS	
ORIGIN	
Alignment Scores:	
Pred. No.:	1.76e-27
Score:	283.00
Percent Similarity:	95.00%
Best Local Similarity:	92.00%
Query Match:	94.02%
DB:	8
Gaps:	0
US-10-006-252A-10 (1-50) x AF528180 (1-363)	
QY	1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db	112 AAGTTGTGCGAGAGGTCTAGTGGGACATGGTCAGAGTATGTGGAATATCAATGCTTGC 171
QY	21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db	172 AAGAACCAGTGCATCACTTGGAGGACGACATGATCTTGCAACTATGTTTCCCA 231
QY	41 AlaHisLysCysIleCysTyrPheProCys 50
Db	232 TATCACAGGTGATCTGCTACTTCCCATGT 261
RESULT 5	
RSAPP4	
LOCUS	RSAPP4 499 bp mRNA linear PLN 31-OCT-1996
DEFINITION	R. sativus mRNA for antifungal protein 4.
ACCESSION	X97318
VERSION	X97318.1 GI:1655682
KEYWORDS	AFP; antifungal protein 4.
SOURCE	Raphanus sativus (radish)
ORGANISM	Raphanus sativus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
REFERENCE	1
AUTHORS	Terras,F.R.G., Godeis,I.J., Penninckx,I.J., Osborn,R.W. and Broekaert,W.F.
JOURNAL	Unpublished

TITLE	Brassica oleracea def gene for defensin
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 933)
AUTHORS	Esnault,R.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2001) Esnault R., Institut des Sciences Vegetales, C.N.R.S., Avenue de la Terrasse, 91 198 Gif sur Yvette cedex, FRANCE
FEATURES	Location/Qualifiers 1..933 /organism="Brassica oleracea" /mol_type="genomic DNA" /db_xref="taxon:3712" /dev_stage="seedlings" 1..829 /gene="def" 1..333 /gene="def" 334..365 /gene="def" Join(366..429,528..>706) Join(366..429,528..706) /gene="def" /functions="involved in plant defense" /codon_start=1 /product="defensin" /protein_id="CAC37558.1" /db_xref="GI:1387214" /db_xref="GOA:Q941N7" /db_xref="SPTREMBL:Q941N7" /translation="MAKVASIVALLFPALVIFPAFEAPTVAQKLCERPSTWSGVC GNNACKQCCIRLEKARHGSCNIVFPARHCICYPFC" Join(366..429,528..550) /gene="def" Join(366..429 366..429 /gene="def" /number=1 430..527 /gene="def" /number=1 528..>706 /gene="def" /number=2 824..829 /gene="def"
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promoter	
5'UTR	
mRNA	
CDS	
sig_peptide	
exon	
intron	
exon	
polyA_signal	
ORIGIN	
Alignment Scores:	
Pred. No.:	3.71e-27
Score:	284.00
Percent Similarity:	96.00%
Best Local Similarity:	94.00%
Query Match:	94.35%
DB:	8
Gaps:	0
US-10-006-252A-10 (1-50) x BOL311046 (1-933)	
QY	1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db	554 AAGCTGTGCGAAGGCCAAGTGGACGTGTCAGAGTCTGTGGAACATAATGATGC 613
QY	21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db	614 AAGAATCATGTCATTCGACTAGAGAAAGCGCGACATGATCTTGCAACTATGCTTCCCA 673
QY	41 AlaHisLysCysIleCysTyrPheProCys 50
Db	674 GCCCAAGTGCATCTGCTACTTCCCTTGT 703
RESULT 4	
AF528180	
LOCUS	AF528180 363 bp mRNA linear PLN 26-SEP-2002

REFERENCE 2 (bases 1 to 499)
 AUTHORS Terras, F.R.G.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-1996) F.R.G. Terras, Institut fur Pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg 3, Halle (Saale), D-06120, FRG

FEATURES
 source
 1..499
 Location/Qualifiers
 /organism="Raphanus sativus"
 /mol_type="mRNA"
 /cultivar="Ronde Rode Kleine Witpunt"
 /db_xref="taxon:3728"
 /dev_stage="adult plants infected with Alternaria brassicicola"
 gene
 1..499
 /gene="AFP"
 CDS
 44..286
 /gene="AFP"
 /codon_start=1
 /product="antifungal protein 4"
 /protein_id="CAA65983.1"
 /db_xref="GI:1655683"
 /db_xref="GOA:O24331"
 /db_xref="SWISS-PROT:O24331"
 /translation="MAKFSVLIITLLEVALVLEAFETWVEAQKLCERSSTWSGVC
 GNNACKNQINLEGARHGSCNIFPYHRCICFFPC"
 44..130
 /gene="AFP"
 131..283
 /gene="AFP"
 /product="antifungal protein 4"

sig_peptide
 3.37e-27 Length: 499
 282.00 Matches: 45
 Percent Similarity: 96.00%
 Best Local Similarity: 96.00%
 Query Match: 93.69%
 DB: 8 Gaps: 0

mat_peptide
 131..283
 /gene="AFP"
 /product="antifungal protein 4"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.37e-27 Length: 499
 Score: 282.00 Matches: 45
 Percent Similarity: 96.00%
 Best Local Similarity: 96.00%
 Query Match: 93.69%
 DB: 8 Gaps: 0

US-10-006-252A-10 (1-50) x RSAPP4 (1-499)
 QY 1 LysLeuCysGluArgSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
 Db 134 AAGTTGTCGAGAGCTAGTGGACATGTCAGGATGATGGAAATATATCTTGC 193
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 194 AAGAACCAGTGCATCAACCTCGAGGGAGCAGCATGATCTTGCACTATATTTCCCA 253
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 254 TATCACAGGTGATCTGCTACTTCCATGT 283

RESULT 6
 AR014693
 LOCUS Sequence 17 from patent US 5773696.
 DEFINITION AR014693
 ACCESSION AR014693
 VERSION AR014693.1 GI:3972147
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 285)
 AUTHORS Liang, J., Shan, D., Maganlal., Wu, Y., Shun. and Rosenberger, C. Annette.
 TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
 JOURNAL Patent: US 5773696-A 17 30-JUN-1998;
 FEATURES Location/Qualifiers
 source
 1..285
 /organism="unknown"

REFERENCE 2 (bases 1 to 499)
 AUTHORS Terras, F.R.G.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-1996) F.R.G. Terras, Institut fur Pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg 3, Halle (Saale), D-06120, FRG

FEATURES
 source
 1..499
 Location/Qualifiers
 /organism="Raphanus sativus"
 /mol_type="mRNA"
 /cultivar="Ronde Rode Kleine Witpunt"
 /db_xref="taxon:3728"
 /dev_stage="adult plants infected with Alternaria brassicicola"
 gene
 1..499
 /gene="AFP"
 CDS
 44..286
 /gene="AFP"
 /codon_start=1
 /product="antifungal protein 4"
 /protein_id="CAA65983.1"
 /db_xref="GI:1655683"
 /db_xref="GOA:O24331"
 /db_xref="SWISS-PROT:O24331"
 /translation="MAKFSVLIITLLEVALVLEAFETWVEAQKLCERSSTWSGVC
 GNNACKNQINLEGARHGSCNIFPYHRCICFFPC"
 44..130
 /gene="AFP"
 131..283
 /gene="AFP"
 /product="antifungal protein 4"

sig_peptide
 3.37e-27 Length: 499
 282.00 Matches: 45
 Percent Similarity: 96.00%
 Best Local Similarity: 96.00%
 Query Match: 93.69%
 DB: 8 Gaps: 0

mat_peptide
 131..283
 /gene="AFP"
 /product="antifungal protein 4"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.37e-27 Length: 499
 Score: 282.00 Matches: 45
 Percent Similarity: 96.00%
 Best Local Similarity: 96.00%
 Query Match: 93.69%
 DB: 8 Gaps: 0

US-10-006-252A-10 (1-50) x RSAPP4 (1-499)
 QY 1 LysLeuCysGluArgSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
 Db 134 AAGTTGTCGAGAGCTAGTGGACATGTCAGGATGATGGAAATATATCTTGC 193
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 194 AAGAACCAGTGCATCAACCTCGAGGGAGCAGCATGATCTTGCACTATATTTCCCA 253
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 254 TATCACAGGTGATCTGCTACTTCCATGT 283

RESULT 6
 AR014693
 LOCUS Sequence 17 from patent US 5773696.
 DEFINITION AR014693
 ACCESSION AR014693
 VERSION AR014693.1 GI:3972147
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 285)
 AUTHORS Liang, J., Shan, D., Maganlal., Wu, Y., Shun. and Rosenberger, C. Annette.
 TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
 JOURNAL Patent: US 5773696-A 17 30-JUN-1998;
 FEATURES Location/Qualifiers
 source
 1..285
 /organism="unknown"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.44e-27 Length: 285
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00%
 Best Local Similarity: 96.00%
 Query Match: 93.36%
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x AR014693 (1-285)
 QY 1 LysLeuCysGluArgSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
 Db 121 AAGTTGTCGCAAGGCCATCAGGGACTTGTCAGAGTCTGCGGAAACAACAACGATGC 180
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 181 AAGAACCAGTGCATCAGACTCGAGAAGGCAAGCATGATCTTGCACTACGTCTTCCCA 240
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 241 GCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 7
 AR432393
 LOCUS Sequence 17 from patent US 6653280.
 DEFINITION AR432393
 ACCESSION AR432393
 VERSION AR432393.1 GI:40194670
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 285)
 AUTHORS Liang, J., Shan, D.M., Wu, Y.S. and Rosenberger, C.A.
 TITLE Antifungal polypeptide AlyAFP from Alyseum and methods for controlling plant pathogenic fungi
 JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
 FEATURES Location/Qualifiers
 source
 1..285
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.44e-27 Length: 285
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00%
 Best Local Similarity: 96.00%
 Query Match: 93.36%
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x AR432393 (1-285)
 QY 1 LysLeuCysGluArgSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
 Db 121 AAGTTGTCGCAAGGCCATCAGGGACTTGTCAGAGTCTGCGGAAACAACAACGATGC 180
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 181 AAGAACCAGTGCATCAGACTCGAGAAGGCAAGCATGATCTTGCACTACGTCTTCCCA 240
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 241 GCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 8
 A39553
 LOCUS Sequence 41 from Patent WO9416076.
 DEFINITION A39553
 ACCESSION A39553


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VERSION      A39553.1  GI:2295844
KEYWORDS
SOURCE       unidentified
ORGANISM     unidentified
REFERENCE    1 (bases 1 to 288)
AUTHORS      Dubock A.C., Powell, K.A. and Rees, S.B.
TITLE        ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL      ZENECA LTD (GB)
COMMENT      Other publication AU 5820494 940815.
FEATURES     Location/Qualifiers
              1..288
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.:      2.47e-27      Length:      288
Score:          281.00      Matches:    46
Percent Similarity: 96.00%      Conservative: 2
Best Local Similarity: 92.00%      Mismatches: 2
Query Match:    93.36%      Indels:    0
DB:             6           Gaps:          0

US-10-006-252A-10 (1-50) x A39553 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
       133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

Db      133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
       253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 9
LOCUS      AR050161
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION  AR050161
VERSION     AR050161.1  GI:5972153
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
              Terras, F.R.G. and Vanderleyden, J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5824869-A 58 20-OCT-1998;
              Location/Qualifiers
              1..288
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2.47e-27      Length:      288
Score:          281.00      Matches:    46
Percent Similarity: 96.00%      Conservative: 2
Best Local Similarity: 92.00%      Mismatches: 2
Query Match:    93.36%      Indels:    0
DB:             6           Gaps:          0

US-10-006-252A-10 (1-50) x AR050161 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
       133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

Db      133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
       253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 11
LOCUS      123736
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  123736
VERSION     123736.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
              Terras, F.R.G. and Vanderleyden, J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5538525-A 58 23-JUL-1996;
              Location/Qualifiers
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               /mol_type="unassigned DNA"

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Alignment Scores:
Pred. No.:      2.47e-27      Length:      288
Score:          281.00      Matches:    46
Percent Similarity: 96.00%      Conservative: 2
Best Local Similarity: 92.00%      Mismatches: 2
Query Match:    93.36%      Indels:    0
DB:             6           Gaps:          0

US-10-006-252A-10 (1-50) x AR050161 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
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QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

Db      133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
       253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 10
LOCUS      AR130280
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION  AR130280
VERSION     AR130280.1  GI:14118177
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
              Terras, F.R.G. and Vanderleyden, J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 6187904-A 58 13-FEB-2001;
              Location/Qualifiers
              1..288
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ORIGIN
Alignment Scores:
Pred. No.:      2.47e-27      Length:      288
Score:          281.00      Matches:    46
Percent Similarity: 96.00%      Conservative: 2
Best Local Similarity: 92.00%      Mismatches: 2
Query Match:    93.36%      Indels:    0
DB:             6           Gaps:          0

US-10-006-252A-10 (1-50) x AR130280 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
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QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

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QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
       253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 11
LOCUS      123736
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  123736
VERSION     123736.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
              Terras, F.R.G. and Vanderleyden, J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5538525-A 58 23-JUL-1996;
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ORIGIN

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Db      133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

Db      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
       253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 10
LOCUS      AR130280
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION  AR130280
VERSION     AR130280.1  GI:14118177
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
              Terras, F.R.G. and Vanderleyden, J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 6187904-A 58 13-FEB-2001;
              Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      2.47e-27      Length:      288
Score:          281.00      Matches:    46
Percent Similarity: 96.00%      Conservative: 2
Best Local Similarity: 92.00%      Mismatches: 2
Query Match:    93.36%      Indels:    0
DB:             6           Gaps:          0

US-10-006-252A-10 (1-50) x AR130280 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTyrSerGlyValCysGlyAsnAsnAlaCys 20
       133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

Db      133  AAGTTGTGCCAAGGCCAAGTGGACATGGTTCAGGAGTCTGTGGAAACAATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
       193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGTTCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
       253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 11
LOCUS      123736
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  123736
VERSION     123736.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
              Terras, F.R.G. and Vanderleyden, J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5538525-A 58 23-JUL-1996;
              Location/Qualifiers
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ORIGIN

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ORIGIN

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 Best Local Similarity: 92.00% Mismatches: 2
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 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 191 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACATGGTCTTTGCAACTATGCTTCCCA 250

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 251 GCTCAAGTGTATCTGTTATTCCCTTGT 280

RESULT 15

RSU18556 457 bp mRNA linear PLN 07-JUL-1995
 LOCUS Raphanus sativus antifungal protein 2 preprotein (Rs-AFP2) mRNA,
 DEFINITION complete cds.

ACCESSION U18556

VERSION U18556.1 GI:609319

KEYWORDS

SOURCE Raphanus sativus (radish)

ORGANISM

Raphanus sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

REFERENCE

AUTHORS Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
 Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
 Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
 Small cysteine-rich antifungal proteins from radish: their role in
 host defense

JOURNAL Plant Cell 7, 568-573 (1995)

REFERENCE 2 (bases 1 to 457)

AUTHORS

Terras,F.R.

TITLE

Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
 of Genetics, Applied Biological Sciences, W. De Croylaan 42,
 Heverlee, Belgium, B-3001

FEATURES

source

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/mol_type="mRNA"

/strain="Ronde rode kleine witpunt"

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129..281

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mat_peptide

/product="antifungal protein 2"

/function="antifungal, fungistatic"

/note="Evidence for antifungal activity: Analysis of two
 novel classes of antifungal proteins from radish (Raphanus
 sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
 Chem. 267, 15301-15309"

/citation=[1]

/evidence=experimental

ORIGIN

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 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 8 Gaps: 0

US-10-006-252A-10 (1-50) x RSU18556 (1-457)

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Db 132 AAGTTGGTTCAGAGGCCAAGTGGACATGCTCAGGAGTCTTGGAATATTAACGATGC 191

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 192 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACATGGTCTTGCAACTATGCTTCCCA 251

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 252 GCTCAAGTGTATCTGTTATTCCCTTGT 281

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Job time : 1735 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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1	281	93.4	261	2	AaQ38652 Rs-AFP2 c
2	281	93.4	288	2	AaQ70130 Antimicro
3	281	93.4	308	2	AaT94577 Cloned 5'
4	281	93.4	449	3	AaA53190 Raphanus
5	281	93.4	522	3	AaZ99324 DNA encod
6	281	93.4	534	3	AaZ51396 Portion o
7	281	93.4	534	3	AaZ99327 DNA encod
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9	281	93.4	606	3	AaZ99326 DNA encod
10	279	92.7	243	6	AaQ82590
11	279	92.7	394	9	AaC51221 Brassica
12	279	92.7	414	2	AaQ38650
13	279	92.7	414	2	AaQ70128 Antimicro
14	279	92.7	414	2	AaT72333 Raphanus
15	279	92.7	414	2	AaT68696 Radish an
16	279	92.7	414	3	AaZ39123 Wasabia j
17	279	92.7	426	9	AaC51223 Brassica
18	274	91.0	243	6	AaQ82591
19	274	91.0	243	7	AaA68378 Arabidops
20	274	91.0	243	2	AaV10632 A. thalia
21	274	91.0	416	3	AaZ39124 Arabidops
22	272	90.4	243	6	AaZ14241 Arabidops
23	272	90.4	243	7	AaZ42136 Arabidops
24	272	90.4	400	2	AaV10633 A. thalia
25	272	90.4	1616	2	AaV10646 A. thalia
26	270	89.7	485	3	AaZ99337 DNA encod
27	267	88.7	270	2	AaT94582 Amplified
28	267	88.7	286	2	AaT94574 Alyssum s
29	267	88.7	481	2	AaT99289 Alyssum s
30	266	88.4	434	3	AaZ99332 DNA encod
31	266	88.4	437	3	AaZ99331 DNA encod
32	266	88.4	443	3	AaZ99330 DNA encod
33	266	88.4	446	3	AaZ99329 DNA encod
34	266	88.4	485	3	AaZ99333 DNA encod
35	266	88.4	485	3	AaZ99335 DNA encod
36	266	88.4	488	3	AaZ99338 DNA encod
37	266	88.4	557	3	AaZ99336 DNA encod
38	266	88.4	575	3	AaZ99339 DNA encod
39	266	88.4	1093	3	AaZ99334 DNA encod
40	264	87.7	500	2	AaT94581 Composite
41	228	75.7	1973	3	AaC46924 Arabidops
42	208	69.1	284	2	AaQ38651 Truncated
43	208	69.1	284	2	AaQ70129 Antimicro
44	207	68.8	306	2	AaT94580 Cloned 3'
45	162	53.8	150	2	AaQ38644 Encodes a

ALIGNMENTS

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ID AaQ38652 standard; DNA; 261 BP.

XX AC AaQ38652;
XX AC AaQ38652;
DT 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX RS-AFP2 cDNA.
XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.

XX OS Raphanus sativus.
XX Key Location/Qualifiers
FT CDS 16..256
FT FT /*tag= a

XX PN WO9305153-A1.
XX PD 18-MAR-1993.
XX PF 27-AUG-1992; 92WO-GB001570.
XX PR 29-AUG-1991; 91GS-00018523.
PR 13-FEB-1992; 92GB-00003038.
PR 25-JUN-1992; 92GB-00013526.
XX (ICIL) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX WPI; 1993-100978/12.
 XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX Example 21; Fig 35; 110pp; English.
 XX This cDNA represents the sequence of Rs-APP2 from *Raphanus sativus*. PCR
 CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
 CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC K408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence was identified
 CC as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
 CC from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
 CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,51e-26 Length: 261
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservativeness: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 2 Gaps: 0
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 QY 1 LysLeuCysGluArgSerSerGlyThrTpsSerGlyValCysGlyAsnAsnAlaCys 20
 Db 106 AAGTTGTGCCAAGGCCAAGTGGACATGTCAGAGTCTGTGGAAACAATAACGCATGC 165
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 166 AAGAATCAGTGCATTAGACTTGAGAAAGCAGCAGCATGATCTTGCAACTATGTCTTCCCA 225
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 226 GCTCACAGTGTATCTGCTACTTCTTGT 255
 RESULT 2
 AAQ70130
 ID AAQ70130 standard; cDNA; 298 BP.
 AC AAQ70130;
 XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX Antimicrobial Rs-APP2.
 XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
 KW Clavibacter xyli subsp. cynodentis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis; ss.
 XX *Raphanus sativus*.
 OS

XX WO9416076-A1.
 PN 21-JUL-1994.
 XX 05-JAN-1994; 94WO-GB0000012.
 PF 08-JAN-1993; 93GB-00000281.
 PR (ZENE) ZENECA LTD.
 PA Dubock AC, Powell KA, Rees SB,
 PI WPI; 1994-249223/30.
 XX P-PSDB; AAR57327.
 DR Antimicrobial protein producing endo-symbiotic microorganisms - is
 CC produced by combining nucleic acids encoding the protein with an
 CC endophyte, useful for protecting plant hosts from esp. fungal disease.
 PT Disclosure; Page 33; 39pp; English.
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyli subsp. cynodentis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APP1 from *R. sativus*. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
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 Pred. No.: 3,98e-26 Length: 288
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 Percent Similarity: 96.00% Conservativeness: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 2 Gaps: 0
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 QY 1 LysLeuCysGluArgSerSerGlyThrTpsSerGlyValCysGlyAsnAsnAlaCys 20
 Db 133 AAGTTGTGCCAAGGCCAAGTGGACATGTCAGAGTCTGTGGAAACAATAACGCATGC 192
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 193 AAGAATCAGTGCATTAGACTTGAGAAAGCAGCAGCATGATCTTGCAACTATGTCTTCCCA 252
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 253 GCTCACAGTGTATCTGCTACTTCTTGT 282
 RESULT 3
 AAT94577
 ID AAT94577 standard; DNA; 308 BP.
 AC AAT94577;
 XX 12-MAY-1998 (first entry)
 DT Cloned 5' region of antifungal polypeptide cDNA.
 XX Antifungal polypeptide; AlyAPP; inhibition; transgenic plants;
 KW phytopathogenic fungus; resistance; ss.
 XX *Alyssum* sp.
 OS WO9737024-A2.
 PN 09-OCT-1997.
 PD

PF 27-MAR-1997; 97WO-US0005709.
 XX
 PR 29-MAR-1996; 96US-00627706.
 XX
 PA (MONS) MONGANTO CO.
 XX
 PI Liang J, Shah D, Wu Y, Rosenberger CA;
 XX WPI; 1997-503109/46.
 DR
 XX
 PT Alyssum antifungal polypeptide and corresponding DNA - used in the
 XX production of transgenic plants resistant to phytopathogenic fungi.
 PT
 PS Example 4; Page 65; 92pp; English.
 XX
 CC This sequence is the product of the amplification of the 5' region of the
 CC antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum,
 CC by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAT94575-
 CC T94576). The AlyAFP polypeptide can be used to control phytopathogenic
 CC fungi, whilst the coding DNA can be used to produce transgenic plants
 CC that express the polypeptide making them resistant to the phytopathogenic
 CC fungi
 XX
 SQ Sequence 308 BP; 78 A; 71 C; 78 G; 79 T; 0 U; 2 Other;
 Alignment Scores: Length: 308
 Pred. No.: 4.34e-26 Matches: 46
 Score: 281.00
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 92.00% Mismatches: 3
 Query Match: 93.36% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-10 (1-50) x AAT94577 (1-308)
 QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 159 AAGTTGTGCGAGAGTCCCAAGTGAACATGTCAGGCGTGTGTGGAACACAAATGCTGC 218
 QY 21 LysAsnGlnCysIleArgLeuGluGluValAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 219 AAGATCATGTCATTAACTTGAAGAGCGACATGATCTTGCACATATGCTCTCCCA 278
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 279 GCTCACAAGTGCATATGCTACTTCCCTGT 308
 RESULT 4
 ID AAA53190 standard; DNA; 449 BP.
 AC AAA53190;
 XX
 DT 06-OCT-2000 (first entry)
 DE
 DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
 KW pathogenic microbe; radish; rice blast disease; ds.
 OS Raphanus sativus.
 OS
 XX JP2000116379-A.
 XX
 XX 25-APR-2000.
 XX
 XX 09-OCT-1998; 98JP-00288472.
 XX
 XX 09-OCT-1998; 98JP-00288472.
 XX
 XX (TOYA-) TOYAMA KEN.
 XX WPI; 2000-389821/34.
 DR

DR P-PSDB; AAY91117.
 XX
 PT Isolated DNA from Raphanus sativus used to transform a microbe and a
 PT plant to produce an antibacterial protein used to increase resistance of
 PT rice paddy against pathogenic microbes.
 XX
 PS Claim 1; Page 4; 7pp; Japanese.
 XX
 CC The present sequence encodes an antibacterial protein, designated
 CC radishin, isolated from Raphanus sativus (radish). A phage or plasmid
 CC comprising radishin can be used for increasing resistance of paddy and
 CC rice blast disease against pathogenic microbes
 XX
 SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
 Alignment Scores: Length: 449
 Pred. No.: 7.02e-26 Matches: 46
 Score: 281.00
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-10 (1-50) x AAA53190 (1-449)
 QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 131 AAGTTGTGTCAGAGGCCACAGTGGGACATGTCAGGAGTCTGTGGAATATAACGATGC 190
 QY 21 LysAsnGlnCysIleArgLeuGluGluValAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 191 AAGATCATGTCATTGACCTTGAGAAAGCAGCATGGTCTTGCACATATGCTCTCCCA 250
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 251 GCTCACAAGTGCATATGCTACTTCCCTGT 280
 RESULT 5
 ID AAA53190 standard; DNA; 522 BP.
 AC AAA53190;
 XX
 DT 03-JUL-2000 (first entry)
 DE
 DE DNA encoding a fusion protein of DnaMpi and RsAPP2.
 KW Antimicrobial protein; AMPI; transgenic plant; linker peptide;
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
 OS Synthetic.
 OS Dahlia merckii.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FT misc_feature 160..309
 FT /tag= a
 FT /note= "encodes DnaMpi"
 FT misc_feature 358..510
 FT /tag= b
 FT /note= "encodes RsAPP2"
 XX
 XX WO200011175-A1.
 XX
 XX 02-MAR-2000.
 XX
 XX 17-AUG-1999; 99WO-GB002716.
 XX
 XX 18-AUG-1998; 98GB-00018001.
 XX 04-DEC-1998; 98GB-00026753.
 XX
 XX (ZENE) ZENECA LTD.
 XX

PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
 XX WPI; 2000-246564/21.
 DR P-PSDB; AAY84057.
 XX
 PT Improving expression of polyproteins in plants involves coexpression of
 PT two or more proteins in plants within a single transcription unit.
 XX
 PS Example 2; Fig 8; 151pp; English.
 XX
 CC The present sequence encodes a protein of the invention, comprising the
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
 CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
 CC propeptide of the invention. The specification describes methods for
 CC improving expression levels of one or more proteins in a transgenic
 CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 CC comprising a cleavage site, whereby the expressed polypeptide is post-
 CC translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptide sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence
 XX
 SQ Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.51e-26 Length: 522
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-10 (1-50) x AAZ99324 (1-522)
 Qy 1 LysLeuGlnCysIleArgSerSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 361 AAGTTGTCGCAAGGCCAAGTGGACATGTCAGAGTCCTGCGAACAATACCGCATGC 420
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 421 AAGAATCAGTGCATTAGACTTGAGAAAGCAGACATGGATCTTGGCACTATGCTTCCCA 480
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 481 GCTCACAAGTGTATCTGCTACTTTCCTTGT 510
 RESULT 6
 AAZ51396
 ID AAZ51396 standard; DNA; 534 BP.
 XX
 AC AAZ51396;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.
 KW Antimicrobial protein; DmAMP; transgenic plant; microbial infection;
 KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;
 KW apple; plant transformation vector; ds.
 XX
 OS Dahlia merckii.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..525
 FT /*tag= a
 FT /product= "Antimicrobial protein"
 XX
 PN W0200011196-A1.
 XX

PD 02-MAR-2000.
 XX
 PF 17-AUG-1999; 99WO-GB002720.
 XX
 PR 18-AUG-1998; 98GB-00018003.
 XX
 PA (ZENNE) ZENECA LTD.
 XX
 PI Evans IJ, Ray JA;
 XX
 DR WPI; 2000-237658/20.
 DR P-PSDB; AAY70323.
 XX
 PT Polynucleotide sequences and expression products useful for producing
 PT transgenic plants that are resistant to microbial infections.
 XX
 PS Example 3; Fig 7; 77pp; English.
 XX
 CC The present sequence corresponds to the region between XhoI and SacI
 CC sites of plant transformation vector pFAJ3106, which encompass the coding
 CC region for Dahlia merckii antimicrobial protein, Dm-AMP1. The vector is
 CC useful in the production of transgenic plants which show improved
 CC resistance to infections by microorganisms such as bacteria and fungi.
 CC Transgenic plants include e.g. field crops, fruits and vegetables, such
 CC as canola, sunflower, tomato, apple, banana, pear and mango
 XX
 SQ Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.76e-26 Length: 534
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-10 (1-50) x AAZ51396 (1-534)
 Qy 1 LysLeuGlnCysIleArgSerSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 373 AAGTTGTCGCAAGGCCAAGTGGACATGTCAGAGTCCTGCGAACAATACCGCATGC 432
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 433 AAGAATCAGTGCATTAGACTTGAGAAAGCAGACATGGATCTTGGCACTATGCTTCCCA 492
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 493 GCTCACAAGTGTATCTGCTACTTTCCTTGT 522
 RESULT 7
 AAZ99327
 ID AAZ99327 standard; DNA; 534 BP.
 XX
 AC AAZ99327;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
 XX
 OS Synthetic.
 OS Dahlia merckii.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..522
 FT /*tag= a
 FT misc_feature 162..309
 FT /*tag= b
 FT /note= "encodes DmAMP1"
 FT


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FT misc_feature 372..519
FT FT /*tag= c
FT FT /note= "encodes RsAPP2"
XX PN WO200011175-A1.
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX PA (ZENE ) ZENECA LTD.
XX XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX XX WPI; 2000-246564/21.
XX XX P-PSDB; AAY84060.
XX FT Improving expression of polyproteins in plants involves coexpression of
XX FT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 12; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 534 BP; 154 A; 120 C; 125 G; 135 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.76e-26 Length: 534
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservativeness: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x AAZ99327 (1-534)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 373 AAGTTGTGCCAAGGCCCAAGTGGGACATGTCAGGAGTCGTGGAACCAATACGATGC 432

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 433 AAGATCATGTCATAGACTTGAAGAAGCAGCAGCATGATGCTTGCACACTATGCTTCCCA 492

QY 41 AlahisLysCysIleCysTyrPheProCys 50
DB 493 GCTCACAGTGTATCTGCTACTTTCCTTGT 522

RESULT 8
AAZ99325
ID AAZ99325 standard; DNA; 534 BP.
XX AC AAZ99325;
XX XX
DT 03-JUL-2000 (first entry)
XX XX
DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.

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XX XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX OS Synthetic.
XX OS Dahlia merckii.
XX OS Unidentified.
XX XX Key Location/Qualifiers
XX FT CDS 76..522
XX FT /*tag= a
XX FT misc_feature 160..309
XX FT /*tag= b
XX FT /*note= "encodes DmAMP1"
XX FT misc_feature 370..538
XX FT /*tag= c
XX FT /*note= "encodes RsAPP2"
XX PN WO200011175-A1.
XX PD 02-MAR-2000.
XX XX 17-AUG-1999; 99WO-GB002716.
XX XX 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX XX (ZENE ) ZENECA LTD.
XX XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX XX WPI; 2000-246564/21.
XX XX P-PSDB; AAY84058.
XX FT Improving expression of polyproteins in plants involves coexpression of
XX FT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 9; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.76e-26 Length: 534
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservativeness: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x AAZ99325 (1-534)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 373 AAGTTGTGCCAAGGCCCAAGTGGGACATGTCAGGAGTCGTGGAACCAATACGATGC 432

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 433 AAGATCATGTCATAGACTTGAAGAAGCAGCAGCATGATGCTTGCACACTATGCTTCCCA 492

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Qy 41 AlahisLysCysileCysTyrPheProCys 50
 |||||
 Db 493 GCTCACAGTGATCTGCTACTTCTTGT 522

RESULT 9
 AAZ99326

ID AAZ99326 standard; DNA; 606 BP.
 AC AAZ99326;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
 XX Synthetic.
 OS Dahlia merckii.
 OS Unidentified.

PH Key Location/Qualifiers
 FT CDS 76..597
 FT /*tag= a
 FT misc_feature 160..309
 FT /*tag= b
 FT /*note= "encodes DmAMP1"
 FT misc_feature 442..594
 FT /*tag= c
 FT /*note= "encodes RsAFP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

XX 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84059.

XX Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

XX Example 2; Fig 11; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence

XX Sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.03e-25 Length: 606
 Score: 281.00 Matches: 46

Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x AAZ99326 (1-606)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 |||||
 Db 445 AAGTTGTGCCAAAGGCCAAGTGGACATGGTCAGAGTCTGTGGAACAATAACGCATGC 504
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 505 AAGATCAGTCATTAGACTTGGAGAACGACACATGGATCTTGCAACTATGTTCTCCCA 564
 Qy 41 AlahisLysCysileCysTyrPheProCys 50
 |||||
 Db 565 GCTCACAGTGATCTGCTACTTCTTGT 594

RESULT 10

ABQ82690
 ID ABQ82690 standard; cDNA; 243 BP.

XX AC ABQ82690;

XX DT 02-JAN-2003 (first entry)

XX DE Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.

XX KW Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene; ss.

XX OS Eutrema wasabi.

XX FH Key Location/Qualifiers

XX CDS 1..243
 FT /*tag= a
 FT /product= "gamma-thionin"

XX JF2002272292-A.

XX 24-SEP-2002.

XX 22-MAR-2001; 2001JP-00083526.

XX 22-MAR-2001; 2001JP-00083526.

XX (IWAT-) IWATE KEN.

XX WPI; 2002-718704/78.

XX P-PSDB; ABP53725.

XX A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.

XX Claim 3; Page 8; 11pp; Japanese.

XX The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present invention

XX Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5.69e-26 Length: 243
 Score: 279.00 Matches: 44
 Percent Similarity: 96.00% Conservative: 4
 Best Local Similarity: 88.00% Mismatches: 2
 Query Match: 92.69% Indels: 0
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x ABQ82690 (1-243)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 91 AAGTTGGCGAGAGTCAAGTGGACATGGTCAGGAGTCTGTGGAAACAACAATCGTGC 150
 Qy 21 LysAsnGlnCysLeuArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 151 AAGAATCAGTGCATCAACCTTGAGGAGCAGCATGGATCTTGCACTATATCTTCCCA 210
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 211 TATCACAGATGATCTGTTACTTCCCATGT 240

RESULT 11

ID ADCS1221 standard; DNA; 394 BP.

AC ADCS1221;

XX 18-DEC-2003 (first entry)

XX Brassica oleracea defensin protein coding sequence.

XX antimicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight; gene; ds.
 KW Brassica oleracea.

OS Brassica oleracea.

XX Key Location/Qualifiers

FH 1. .243

FT CDS /tag= a

FT /product= "Brassica oleracea defensin protein"

XX JP2003088379-A.

XX 25-MAR-2003.

XX 18-SEP-2001; 2001JP-00283117.

XX 18-SEP-2001; 2001JP-00283117.

XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.

XX P-PSDB; ADCS1222.

XX Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.

XX Claim 3; SEQ ID NO 1; 34pp; Japanese.

XX The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present DNA sequence encodes a
 CC Brassica defensin protein of the invention.

XX SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.06e-25 Length: 394

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x ADCS1221 (1-394)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 91 AAGTTGGCGAGAGTCAAGTGGACATGGTCAGGAGTCTGTGGAAACAACAATCGTGC 150

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 151 AAGAATCAGTGCATTAACCTTGAGAAAGCAGCATGGATCTTGCACACTATGTCTTCCCA 210

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 211 GCTCACAGTGTATTTGCTACTTCCCTTGT 240

RESULT 12

ID AAQ38650 standard; DNA; 414 BP.

XX AAQ38650;

XX 25-MAR-2003 (revised)

XX 07-JUL-1993 (first entry)

XX RS-AFP1 cDNA.

XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 KW fungicide; bactericide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.

XX Raphanus sativus.

XX Key Location/Qualifiers

FH 16. .256

FT CDS /tag= a

XX WO9305153-A1.

XX 18-MAR-1993.

XX 27-AUG-1992; 92WO-GB001570.

XX 29-AUG-1991; 91GB-00018523.

XX 13-FEB-1992; 92GB-00003038.

XX 25-JUN-1992; 92GB-00013526.

XX (ICIL) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX WPI; 1993-100978/12.

XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX Example 21; Fig 35; 110pp; English.

XX This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR
 CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
 CC screening a Raphanus sativus seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 14bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage

CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence is given here.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
SQ (Updated on 25-MAR-2003 to correct PN field.)

Alignment Scores:
Pred. No.: 1.12e-25 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-10 (1-50) x AAQ38650 (1-414)

OY 1 LysLeuCySGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 106 AAGTTGTGCGAAGGCCCAAGTGGGACATGCTCAGGAGTCTGTGGAAACAATAACGCATGC 165
OY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyValPhePro 40
DB 166 AAGAATCAGTGCAATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
OY 41 AlahisLysCysIleCysTyPheProCys 50
DB 226 GCTCACAAGTGATCTGCTACTTCTTGT 255

RESULT 13
AAQ70128
ID AAQ70128 standard; cDNA; 414 BP.

XX AC AAQ70128;
XX DT 25-MAR-2003 (revised)
XX DT 14-FEB-1995 (first entry)
XX DE Antimicrobial Rs-AFP1.
XX KW Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance;
XX KW Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX OS Raphanus sativus.
XX PN WO9416076-A1.
XX PD 21-JUL-1994.
XX EF 05-JAN-1994; 94WO-GB0000012.
XX PR 08-JAN-1993; 93GB-00000281.
XX PA (ZENE) ZENECA LTD.
XX PI Dubock AC, Powell KA, Rees SB;
XX DR WPI; 1994-249223/30.
XX DR P-PSDB; AAR57325.

XX PT Antimicrobial protein producing endo-symbiotic microorganisms - is
XX PT produced by combining nucleic acids encoding the protein with an
XX PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX PS Disclosure; Page 31; 39pp; English.
XX CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
XX CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
XX CC recombinant Cxc are protected against fungal disease. A suitable
XX CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA
XX CC sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to

CC correct PN field.)
XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
SQ (Updated on 25-MAR-2003 to correct PN field.)

Alignment Scores:
Pred. No.: 1.12e-25 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 2 Gaps: 0

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OY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyValPhePro 40
DB 166 AAGAATCAGTGCAATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
OY 41 AlahisLysCysIleCysTyPheProCys 50
DB 226 GCTCACAAGTGATCTGCTACTTCTTGT 255

RESULT 14
AAQ72333
ID AAQ72333 standard; cDNA; 414 BP.

XX AC AAQ72333;
XX DT 25-MAR-2003 (revised)
XX DT 19-JAN-1998 (first entry)
XX DE Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
XX KW Antifungal protein; candida; fungal resistance; food additive; radish;
XX KW crop protection; plant defensin; bacterial protection; preservative; ss.
XX OS Raphanus sativus.

XX PH Key Location/Qualifiers
XX FT CDS 16..258
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XX FT /transl_except= (pos:85..87, aa:Glu)
XX FT sig_peptide 16..102
XX FT /*tag= b
XX FT mat_peptide 103..255
XX FT /*tag= c
XX FT /product= "antifungal_protein_1"

XX PN WO9721815-A2.
XX PD 19-JUN-1997.
XX EF 12-DEC-1996; 96WO-GB003068.
XX PR 13-DEC-1995; 95GB-00025455.
XX PR 28-MAR-1996; 96GB-00006552.
XX PA (ZENE) ZENECA LTD.
XX PI Meleen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
XX PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX PI Van Gelder WMJ;
XX DR WPI; 1997-332786/30.
XX DR P-PSDB; AAM19280.

XX PT Antifungal peptide derived from radish antifungal protein 2 - and related
XX PT DNA, useful for producing plants with increased fungal resistance and as
XX PT therapeutic or preservative agent.

XX PS Claim 8; Fig 2; 65pp; English.

XX CC This cDNA sequence encodes an Raphanus sativus (radish) antifungal

XX CC protein (Rs-APP1). Analogues of the homologous protein, Rs-APP2

XX CC (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,

XX CC AAW19301-04, AAW19330-34 and AAW31765-834). Plants containing DNA

XX CC sequences encoding these proteins have improved resistance to fungi.

XX CC Compositions containing the peptides can be used to control fungi or

XX CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or

XX CC preservative purposes (as food additives). In agriculture, the peptide

XX CC may be used to improve disease resistance or disease tolerance of crops,

XX CC either pre or post harvest. When applied to plants they may also have

XX CC curative as well as protective actions. The peptides may also be used to

XX CC protect plants by introducing them, or a microorganism capable of

XX CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct

XX CC PI field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,12e-25	Length:	414
Score:	279.00	Matches:	46
Percent Similarity:	94.00%	Conservative:	1
Best Local Similarity:	92.00%	Mismatches:	3
Query Match:	92.69%	Indels:	0
DB:	2	Gaps:	0

US-10-006-252A-10 (1-50) x AAT72333 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGGAAAGCCAAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGATCAGTGCATTAACTTGGAGAACGACGACATGATGCTTGCACATGCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAGTGTATCTGCTACTTCTTGT 255

RESULT 15

ID AAT68696

AC AAT68696 standard; cDNA; 414 BP.

XX AC AAT68696;

XX DT 13-DEC-1997 (first entry)

XX DE Radish antifungal protein 1 (Rs-APP1) cDNA.

XX KW Rs-APP1; radish antifungal protein 1; fungicide; salt tolerance;

XX KW preservative; transgenic plant; crop protection.

XX OS Raphanus sativus.

XX FH Key	Location/Qualifiers
XX FT CDS	16..258
XX FT	/*tag= a
XX FT	/*trans_except= (pos:85..87, aa:Glu)
XX FT	16..102
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XX PN WO9721814-A1.

XX PD 19-JUN-1997.

XX PF 12-DEC-1996; 96WO-GB003065.

XX PR 13-DEC-1995; 95GB-00025474.

XX PA

(ZENE) ZENECA LTD.

XX PI Broekaert WF, De Samblaux GW, Rees SB;

XX DR WPI: 1997-332785/30.

XX DR P-PSDB; AAW19617.

XX PT New active mutants of radish antifungal protein 2 - used to generate

XX PT fungus-resistant plants or as therapeutic or preservative agents.

XX PS Disclosure; Fig 2; 39pp; English.

XX CC This cDNA clone codes for the preprotein for radish antifungal protein 1

XX CC (Rs-APP1) (AAW19617). Novel antifungal proteins are based on Rs-APP1, Rs-

XX CC APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9

XX CC is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by

XX CC Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The

XX CC mutants show improved salt tolerant antifungal activity, particularly

XX CC when expressed in plants

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,12e-25	Length:	414
Score:	279.00	Matches:	46
Percent Similarity:	94.00%	Conservative:	1
Best Local Similarity:	92.00%	Mismatches:	3
Query Match:	92.69%	Indels:	0
DB:	2	Gaps:	0

US-10-006-252A-10 (1-50) x AAT68696 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGGAAAGCCAAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 165

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGATCAGTGCATTAACTTGGAGAACGACGACATGATGCTTGCACATGCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAGTGTATCTGCTACTTCTTGT 255

Search completed: May 13, 2004, 11:06:38

Job time : 350 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 10:54:53 ; Search time 85 Seconds
(without alignments)
326.442 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

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Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	281	93.4	288	1	US-08-829-381D-17
6	281	93.4	288	1	Sequence 58, Appl
7	281	93.4	288	3	US-08-377-687-58
8	281	93.4	308	1	US-08-777-192-58
9	281	93.4	308	1	Sequence 58, Appl
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34	162	53.8	150	1	US-08-777-192-31	Sequence 31, Appl
35	162	53.8	150	3	US-08-971-982-31	Sequence 31, Appl
36	159	52.8	150	1	US-08-377-687-34	Sequence 34, Appl
37	159	52.8	150	1	US-08-777-192-34	Sequence 34, Appl
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ALIGNMENTS

RESULT 1
US-08-627-706-17
; Sequence 17, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 17:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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RESULT 2
US-09-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-17
Alignment Scores:
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Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservatives: 2
Best Local Similarity: 92.00% Mismatches: 2
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US-10-006-252A-10 (1-50) x US-09-829-381D-17 (1-285)
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Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-17
Alignment Scores:
Pred. No.: 3 12e-28 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservatives: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
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Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAGAAGCGACGCGATGATCTTGCAACTACGTCTTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 2
US-09-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; FILE REFERENCE: 38-21 (10700) A
; CURRENT APPLICATION NUMBER: 38-21 (10700) A
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700) A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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RESULT 4

US-08-377-687-58
 ; Sequence 58, Application US/08377687
 ; Patent No. 5538525
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKAERT, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERRAS, FRANKY R.G.
 ; APPLICANT: VANDERLEVDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/377,687
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
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 ; NAME/KEY: CDS
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 US-08-377-687-58

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RESULT 5

US-08-777-192-58
 ; Sequence 58, Application US/08777192
 ; Patent No. 5824869
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKAERT, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERRAS, FRANKY R.G.
 ; APPLICANT: VANDERLEVDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/777,192
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..282
 ;
 US-08-777-192-58

Alignment Scores:
 Pred. No.: 3.17e-28 Length: 288
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-777-192-58 (1-288)

Qy	1	LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	133	AGTGTGTCACAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACCATGC	192
Qy	21	LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro	40
Db	193	AAGAATCAGTGCATTAGACTTGAGAAAGCAGCATGATCTTGGCAACTATGTTCTTCCCA	252
Qy	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	253	GCACACAGTGTATCTGCTACTTCTTCTTGT	282

RESULT 6

US-08-971-982-58
 ; Sequence 58, Application US/08971982
 ; Patent No. 6187904
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKART, WILLEM F.
 ; CAMMUE, BRUNO P.A.
 ; OSBORN, RUPERT W.
 ; REES, SARAH B.
 ; TERRAS, FRANKY R.G.
 ; VANDERLEYDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARRY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/971,982
 ; FILING DATE: 17-No. 6187904-1997
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..282
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
 ;

US-08-971-982-58

Alignment Scores:
 Pred. No.: 3.17e-28 Length: 288
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-971-982-58 (1-288)

QY	1	LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	133	AAAGTTGGCCAAAGGCCAAGTGGACATGCTGAGAGTCTGGGAAACAATAACGATGC	192
QY	21	LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro	40
Db	193	AAGAATCAGTGCATTAGACTTTGAGAAAGCACGACATGATCTTGCAACTATGCTTCCCA	252
QY	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	253	GCTCACAGGTATCTGCTACTTTCCTTGT	282

RESULT 7

US-08-627-706-5
 ; Sequence 5, Application US/08627706
 ; Patent No. 5773696
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yonnie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 ; Controlling Plant Pathogenic Fungi
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
 ; STREET: 700 Chesterfield Village Parkway No. 5773696th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/627,706
 ; FILING DATE:
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cohen, Charles E.
 ; REGISTRATION NUMBER: 34,565
 ; REFERENCE/DOCKET NUMBER: 38-21(10700)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314)537-6224
 ; TELEFAX: (314)537-6047
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 308 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ;

US-08-627-706-5

Alignment Scores:
 Pred. No.: 3.46e-28 Length: 308
 Score: 281.00 Matches: 46
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 92.00% Mismatches: 3
 Query Match: 93.36% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-627-706-5 (1-308)

QY	1	LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	159	AAAGTTGGCGAGTCCCAAGTGGACATGTCAGCGTGTGTGGAACAACAATGCTTGC	218
QY	21	LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro	40
Db	219	AAGAATCAGTGCATTAACTTTGAAGAGCAGCATGATCTTGCAACTATGCTTCCCA	278
QY	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	279	GCTCAAGTGCATTATGCTTTCCTTGT	308

RESULT 8

US-09-103-489-5
 ; Sequence 5, Application US/09103489
 ; Patent No. 6215048
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong

```

; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-103-489-5

Alignment Scores:
Pred. No.: 3,46e-28 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-103-489-5 (1-308)

QY 1 LysleuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCAGTGAACATGTCAGGCGTGTGTGGAAACAACTGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGGAGCNCAGCATGATCTTGCACACTATGCTCTTCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAGTGCATATGCTACTTCCCTGT 308

RESULT 9
US-09-829-381D-5
; Sequence 5, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALVAPP from Alyesum and Methods for Contro
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D

; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-10-006-252A-10 (1-50) x US-09-103-489-5 (1-308)

QY 1 LysleuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCAGTGAACATGTCAGGCGTGTGTGGAAACAACTGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGGAGCNCAGCATGATCTTGCACACTATGCTCTTCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAGTGCATATGCTACTTCCCTGT 308

RESULT 10
US-08-627-706-16
; Sequence 16, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
```

```
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16

Alignment Scores:
Pred. No.: 5.69e-28 Length: 285
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservaive: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-627-706-16 (1-285)
QY 1 LysLeuCyGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGCGGAACAAACACGATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAACTCGAGAAGCGACGGCATGCTTGCACACTACGTCCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 11
US-09-103-489-16
; Sequence 16, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Charles E. Cohen, Monsanto Company, B84F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-16

Alignment Scores:
Pred. No.: 5.69e-28 Length: 285
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservaive: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-103-489-16 (1-285)
QY 1 LysLeuCyGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGCGGAACAAACACGATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAACTCGAGAAGCGACGGCATGCTTGCACACTACGTCCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 12
US-09-829-381D-16
; Sequence 16, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-16

Alignment Scores:
Pred. No.: 5.69e-28 Length: 285
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservaive: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 4 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381D-16 (1-285)
QY 1 LysLeuCyGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGGTCAGGAGTCTGCGGAACAAACACGATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAACTCGAGAAGCGACGGCATGCTTGCACACTACGTCCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270
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Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 13

US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48

Alignment Scores:
Pred. No.: 9.24e-28 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-377-687-48 (1-414)

Qy 1 LysLeuCysGluArgSerSerglyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAACAATAACGCATGC 165
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAAATCAGTGCATTAAACCTTGAGAAAGCACGACATGGATCTTGGCAACTATGCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAGTGTACTCTGCTACTTTCTTGT 255

RESULT 14

US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-777-192-48

Alignment Scores:
Pred. No.: 9.24e-28 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-777-192-48 (1-414)

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Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAAATCAGTGCATTAAACCTTGAGAAAGCACGACATGGATCTTGGCAACTATGCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 15
US-08-971-982-48
; Sequence 48, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48

Alignment Scores:
Pred. No.: 9.24e-28 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-971-982-48 (1-414)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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QY 21 LysAsnGlnCysIleA-gLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGAATCAGTCATTAACTTTGAGAAACACGACATGATCTTGCACACTATGCTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 11:00:48 ; Search time 3321 Seconds

(without alignments)
68.324 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301
Sequence: 1 KLCERSGTSWGVGNNAAC.....QHGSNYPFAHKICYPFC 50

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Database : Published Applications NA.*

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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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ALIGNMENTS

RESULT 1
US-09-829-381A-17
; Sequence 17, Application US/09829381A
; Patent No. US2002014306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US2002014306A1h
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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3	281	93.4	288	9	US-09-759-584-58	Sequence 58, Appl
4	281	93.4	308	9	US-09-829-381A-5	Sequence 5, Appl
5	281	93.4	308	13	US-10-681-972-5	Sequence 5, Appl
6	279	92.7	285	9	US-09-829-381A-16	Sequence 16, Appl
7	279	92.7	285	13	US-10-681-972-16	Sequence 16, Appl
8	279	92.7	414	9	US-09-759-584-48	Sequence 48, Appl
9	279	92.7	414	13	US-10-388-361A-45	Sequence 45, Appl
10	279	92.7	414	14	US-10-006-252A-19	Sequence 19, Appl
11	274	91.0	403	9	US-09-732-561-13	Sequence 13, Appl
12	272	90.4	243	9	US-09-938-842A-2046	Sequence 2046, Ap
13	272	90.4	243	11	US-09-938-842A-2046	Sequence 2046, Ap
14	272	90.4	400	9	US-09-732-561-15	Sequence 15, Appl
15	272	90.4	400	9	US-09-887-576-607	Sequence 607, App
16	272	90.4	1616	9	US-09-732-561-21	Sequence 21, Appl
17	267	88.7	270	9	US-09-829-381A-14	Sequence 14, Appl
18	267	88.7	270	13	US-10-681-972-14	Sequence 14, Appl
19	267	88.7	286	9	US-09-829-381A-12	Sequence 12, Appl
20	267	88.7	286	13	US-10-681-972-12	Sequence 12, Appl
21	264	87.7	500	9	US-09-829-381A-9	Sequence 9, Appl
22	264	87.7	500	13	US-10-681-972-9	Sequence 9, Appl
23	208	69.1	284	9	US-09-759-584-50	Sequence 50, Appl
24	207	68.8	306	9	US-09-829-381A-8	Sequence 8, Appl
25	207	68.8	306	13	US-10-681-972-8	Sequence 8, Appl
26	167	55.5	373	9	US-09-770-696-283	Sequence 283, Appl
27	165	54.8	579	15	US-10-178-449A-31	Sequence 31, Appl
28	162	53.8	150	9	US-09-759-584-31	Sequence 31, Appl
29	162	53.8	529	15	US-10-178-449A-48	Sequence 48, Appl
30	160	53.2	156	15	US-10-178-449A-34	Sequence 34, Appl
31	160	53.2	250	15	US-10-178-449A-36	Sequence 36, Appl
32	160	53.2	610	15	US-10-178-449A-29	Sequence 29, Appl
33	160	53.2	658	15	US-10-178-449A-7	Sequence 7, Appl
34	159	52.8	150	9	US-09-759-584-34	Sequence 34, Appl
35	158	52.5	439	15	US-10-178-449A-15	Sequence 15, Appl
36	158	52.5	457	15	US-10-178-449A-13	Sequence 13, Appl
37	158	52.5	458	15	US-10-178-449A-21	Sequence 21, Appl
38	158	52.5	461	15	US-10-178-449A-17	Sequence 17, Appl
39	158	52.5	463	15	US-10-178-449A-46	Sequence 46, Appl
40	158	52.5	463	15	US-10-178-449A-9	Sequence 9, Appl
41	158	52.5	472	15	US-10-178-449A-19	Sequence 19, Appl
42	158	52.5	472	15	US-10-178-449A-23	Sequence 23, Appl
43	158	52.5	603	15	US-10-178-449A-11	Sequence 11, Appl
44	157	52.2	150	9	US-09-759-584-33	Sequence 33, Appl
45	154	51.2	585	12	US-10-636-396-6	Sequence 6, Appl

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Alignment Scores:
Pred. No.: 6.96e-31 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381A-17 (1-285)

Qy 1 LysLeuCySGluArgSerSerglyThrTrpSerglyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCAAAAGGCCATCAGGACTTGTCTGAGGAGTCTGGGAAACAAACACCGCATGC 180
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGAGCGACGGCATGATCTTGCAACTACGCTCTTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 2

US-10-681-972-17
Sequence 17, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu Yennie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
PRIOR FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 285
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetic
US-10-681-972-17

Alignment Scores:
Pred. No.: 6.96e-31 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 13 Gaps: 0

US-10-006-252A-10 (1-50) x US-10-681-972-17 (1-285)

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Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGAGCGACGGCATGATCTTGCAACTACGCTCTTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 3

US-09-759-584-58
Sequence 58, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEVDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 43...282
US-09-759-584-58

Alignment Scores:

Pred. No.: 7.06e-31 Length: 288
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 9 Gaps: 0

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Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 193 AAGAATCAGTGCATTAGACTTGAGAAAGCAGCATGGATCTTGCACACTATGTCTTCCCA 252
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 253 GCTCAAGTGTACTCTCTACTTCTCTTGT 282

RESULT 4

US-09-829-381A-5
; Sequence 5, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Applicant: Shah, Dilip M.
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-829-381A-5

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Pred. No.: 7.7e-31 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 9 Gaps: 0

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Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
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Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGAGCNCGACATGGATCTTGCACACTATGTCTTCCCA 278
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCAAGTGCATATGCTACTTCCCGCTGT 308

RESULT 5

US-10-681-972-5
; Sequence 5, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Applicant: Shah, Dilip M.
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Co
; Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 308
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: Synthetic PCR reaction product
; NAME/KEY: misc_feature
; LOCATION: (22)..(248)
; OTHER INFORMATION: N = any nucleotide
US-10-681-972-5

Alignment Scores:

Pred. No.: 7.7e-31 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 13 Gaps: 0

US-10-006-252A-10 (1-50) x US-10-681-972-5 (1-308)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGCGAGAGTCCAAAGTGGACATGCTCAGGCGTGTGTGGAAACAAACAATGCTTGC 218
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGAGCNCGACATGGATCTTGCACACTATGTCTTCCCA 278
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 279 GCTCACAAGTGCATATGCTACTTCCCTGT 308

RESULT 6

US-09-829-381A-16

; Sequence 16, Application US/09829381A

; Patent No. US20020144306A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip M.

; APPLICANT: Wu, Yonnie S.

; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide and Methods for

; Controlling Plant Pathogenic Fungi

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

; CITY: St. Louis

; STATE: Missouri

; COUNTRY: USA

; ZIP: 63198

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/829,381A

; FILING DATE: 09-Apr-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/103,489

; FILING DATE: 1998-06-24

; ATTORNEY/AGENT INFORMATION:

; NAME: Cohen, Charles E.

; REGISTRATION NUMBER: 34,565

; REFERENCE/DOCKET NUMBER: 38-21 (10700)A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (314) 537-6224

; TELEFAX: (314) 537-6047

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 285 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid

; DESCRIPTION: /desc = "synthetic DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-829-381A-16

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381A-16 (1-285)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGGGAAACAAACACCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCAATCAACCTCGAGAGAGCGCATGATCTTGCACACTACGTTCTTCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 7

US-10-681-972-16

; Sequence 16, Application US/10681972

; Publication No. US20040064850A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip M.

; APPLICANT: Wu, Yonnie S.

; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control

; FILE REFERENCE: 38-21 (10700) C

; CURRENT APPLICATION NUMBER: US/10/681,972

; PRIOR FILING DATE: 2003-10-09

; PRIOR APPLICATION NUMBER: US/09/829,381D

; PRIOR FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 09/103,489

; PRIOR FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 16

; LENGTH: 285

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-681-972-16

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-10-681-972-16 (1-285)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGGGAAACAAACACCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCAATCAACCTCGAGAGAGCGCATGATCTTGCACACTACGTTCTTCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

; Sequence 48, Application US/09759584

; Patent No. US20010014732A1

; GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.

; APPLICANT: CAMMUE, BRUNO P.A.

; APPLICANT: OSBORN, RUPERT W.

; APPLICANT: REES, SARAH B.

; APPLICANT: TERRAS, FRANKY R.G.

; APPLICANT: VANDERLEYDEN, JOZEF

; TITLE OF INVENTION: BIOCIDAL PROTEINS

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

Db 106 AAGTTGTCGGAAGCCCAAGTGGACATGCTGAGGAGTCTGTGAAACAAATAACGCATGC 165
Qy 21 LysAsnGlnCysIleA:gluGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCATGTCATTAACCTTGAGAAAGACACATGATCTTGCAACTATGTCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTCCCTGT 255

RESULT 11

US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Wanners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; STRAIN: PFD 1.1

US-09-732-561-13

Alignment Scores:
Pred. No.: 1.09e-29 Length: 403
Score: 274.00 Matches: 45
Percent Similarity: 94.00% Conservative: 2
Best Local Similarity: 90.00% Mismatches: 3
Query Match: 91.03% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-732-561-13 (1-403)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 116 AAGTTGTCGAGAGGCAAGTGGACATGCTCGGAGTTTGGGAAACAGTAACGCGTGC 175
Qy 21 LysAsnGlnCysIleA:gluGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 176 AAGAATCATGTCATTAACCTTGAGAAAGACACATGATCTTGCNACTAATGTCTTCCCA 235
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 236 GCTCACAAGTGTATCTGCTACTTCCCATGT 265

RESULT 12

US-09-938-842A-2046
; Sequence 2046, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2046
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046

Alignment Scores:

Pred. No.: 1.08e-29 Length: 243
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-938-842A-2046 (1-243)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 91 AAGTTGTCGAGAGGCAAGTGGACATGCTCGGAGTTTGGGAAACAGTAATGTCATGC 150
Qy 21 LysAsnGlnCysIleA:gluGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 151 AAGAATCATGTCATTAACCTTGAGAGGACCAACATGATCATGCAACTATGTCTTCCCA 210
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 211 GCACACAAGTGTATCTGTTACGTCCCATGT 240

RESULT 13

US-09-938-842A-2046
; Sequence 2046, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3

;; CURRENT APPLICATION NUMBER: US/09/938,842A
;; CURRENT FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/227,866
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/264,647
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111
;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 2046
;; LENGTH: 243
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046

Alignment Scores:
Pred. No.: 1,08e-29 Length: 243
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 11 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-938-842A-2046 (1-243)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 91 AAGTTGTCGAGAGCAAGTGGACATGTCAGGGGTTTGGGAAACAGTAATGATGC 150
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 151 AAGAAATCAGTGCAATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCCTCCCA 210
QY 41 AlahHisLysCysIleCysTyrPheProCys 50
DB 211 GCACACAAGTGATCTGTTACGTCCTCATGT 240

RESULT 14
US-09-732-561-15
;; Sequence 15, Application US/09732561
;; Patent No. US20020035738A1
;; GENERAL INFORMATION:
;; APPLICANT: Thoma, Bart
;; APPLICANT: Terras, Franky
;; APPLICANT: Penninckx, Iris
;; APPLICANT: Manners, John
;; APPLICANT: Kazan, Kemal
;; APPLICANT: Broekaert, Willem
;; TITLE OF INVENTION: Plant Protection Method
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ZENECA Ag Products
;; STREET: 1800 Concord Pike
;; CITY: Wilmington
;; STATE: DE
;; COUNTRY: USA
;; ZIP: 19850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/732,561
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/202,638
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB97/01672
;; FILING DATE: 20-JUN-1997
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hohenschurtz, Liza D.
;; REGISTRATION NUMBER: 33,712
;; REFERENCE/DOCKET NUMBER: PPD 50165/UST
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (302) 886-1699
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 400 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; ORIGINAL SOURCE:
;; STRAIN: PDF1.2
US-09-732-561-15

Alignment Scores:
Pred. No.: 2,08e-29 Length: 400
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-732-561-15 (1-400)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 122 AAGTTGTCGAGAGCAAGTGGACATGTCAGGGGTTTGGGAAACAGTAATGATGC 181
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 182 AAGAAATCAGTGCAATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCCTCCCA 241
QY 41 AlahHisLysCysIleCysTyrPheProCys 50
DB 242 GCACACAAGTGATCTGTTACGTCCTCATGT 271

RESULT 15
US-09-887-576-607
;; Sequence 607, Application US/09887576
;; Patent No. US20020144047A1
;; GENERAL INFORMATION:
;; APPLICANT: Budworth, P.
;; APPLICANT: Brown, D.
;; APPLICANT: Chang, H.
;; APPLICANT: Zhu, T.
;; APPLICANT: Han, B.
;; APPLICANT: Wang, X.
;; APPLICANT: Cooper, Bret
;; TITLE OF INVENTION: Promoters for regulation of plant expression
;; FILE REFERENCE: 1360.001US1
;; CURRENT APPLICATION NUMBER: US/09/887,576
;; CURRENT FILING DATE: 2001-06-25
;; PRIOR APPLICATION NUMBER: US 60/213,848
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: US 60/214,087
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: US 60/258,692
;; PRIOR FILING DATE: 2000-12-29
;; NUMBER OF SEQ ID NOS: 875
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 607
;; LENGTH: 400
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)..(400)
;; OTHER INFORMATION: n = A,T,C or G
US-09-887-576-607
Alignment Scores:

Pred. No.: 2.08e-29 Length: 400
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-887-576-607 (1-400)

Qy	1	LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	122	AAATTGTGCGAGAGCCAAAGTGGACATGGTCAGGGGTTTGGGAAACAGTAATGCAATGC	181
Qy	21	LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro	40
Db	182	AAGAATCAGTGCATTAACTTGAAGAGGCCAAACATGGATCATGCAACTATGTCTTCCCA	241
Qy	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	242	GCACACAGGTATCTGTACGTCCCATGT	271

Search completed: May 13, 2004, 13:15:13
Job time : 3323 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 10:53:23 ; Search time 2518 seconds
(without alignments)
592.974 Million cell updates/sec

Title: US-10-006-252A-10
Perfect score: 301
Sequence: 1 KLCRRSGTWSGVCNNAC.....QHGSNCYVFAHRCICVFFPC 50

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006252@cgn_1_1_4237@runat_11052004_141948_10963 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- EST.*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: em_gss_hum.*
 - 18: em_gss_inv.*
 - 19: em_gss_pln.*
 - 20: em_gss_vit.*
 - 21: em_gss_fun.*
 - 22: em_gss_mam.*
 - 23: em_gss_mus.*
 - 24: em_gss_pro.*
 - 25: em_gss_rod.*
 - 26: em_gss_phg.*
 - 27: em_gss_vri.*
 - 28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	301	100.0	346	14	CA992140 RC0577 GI
2	284	94.4	409	14	CD832294 EN40.062L
3	284	94.4	425	14	CD834852 EN45.043G
4	284	94.4	427	14	CD833613 EN40.067P
5	284	94.4	449	14	CD833047 EN40.065M
6	284	94.4	457	14	CD831226 EN40.058J
7	284	94.4	473	14	CD834995 EN45.043O
8	284	94.4	476	14	CD833784 EN45.001I
9	284	94.4	476	14	CD834092 EN45.040I
10	284	94.4	481	14	CD833924 EN45.040A
11	284	94.4	482	14	CD833627 EN45.001A
12	284	94.4	523	14	CD833661 EN45.001C
13	284	94.4	543	14	CD828840 EN40.040A
14	284	94.4	543	14	CD830628 EN40.046D
15	284	94.4	646	14	CD829429 EN40.042B
16	284	94.4	762	28	BZ517729 BOMSG66TF
17	281	93.4	721	28	BH473230 EOGXA16TR
18	280	93.0	522	14	CD833938 EN45.040A
19	280	93.0	543	14	CD829085 EN40.041A
20	279	92.7	408	14	CD833779 EN45.001I
21	279	92.7	409	14	CD834090 EN45.040I
22	279	92.7	418	14	CD832625 EN40.064A
23	279	92.7	419	14	CD834168 EN45.040N
24	279	92.7	420	14	CD833944 EN45.040B
25	279	92.7	421	14	CD826491 EN25.064A
26	279	92.7	421	14	CD831111 EN40.058A
27	279	92.7	421	14	CD833977 EN45.040D
28	279	92.7	422	14	CD833983 EN45.040D
29	279	92.7	426	14	CD827413 EN25.067G
30	279	92.7	438	14	CD831294 EN40.058N
31	279	92.7	438	14	CD831479 EN40.059J
32	279	92.7	446	14	CD834068 EN45.040H
33	279	92.7	447	14	CD832592 EN40.063O
34	279	92.7	450	14	CD834611 EN45.042H
35	279	92.7	452	14	CD832071 EN40.061O
36	279	92.7	453	14	CD834008 EN45.040E
37	279	92.7	458	14	CD834994 EN45.043O
38	279	92.7	470	14	CD831680 EN40.060H
39	279	92.7	480	14	CD828332 EN25.070H
40	279	92.7	553	14	CD831014 EN40.047K
41	279	92.7	803	28	BH458392 BOGWE36TF
42	276	91.7	727	28	BH940491 odd80907.
43	275	91.4	457	14	CD831392 EN40.059D
44	274	91.0	358	9	AA713157 32717 lam
45	274	91.0	421	9	AV816118 AV816118

ALIGNMENTS

RESULT 1
CA992140
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA992140
HC0577 GIBCOBRL CAT. NO. 19643-014
cdNA, mRNA sequence.

CA992140
GI:37621435

EST.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

346 bp mRNA linear EST 10-OCT-2003
Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 346)
 AUTHORS Gao,R.J., Dai,D.P. and Ma,R.C.
 TITLE Expressed sequence tags of heading leaf during the heading process of Chinese cabbage
 JOURNAL Unpublished (2003)
 COMMENT Contact: Kongcai, Ma
 Plant Functional Genomics
 Beijing Agrobiotechnology Research Center
 Haidian District, Ban-Jing Rd., Beijing 100089, China
 Tel: 86 10 5150 3831
 Fax: 86 10 5150 3980
 Email: rcmai@yahoo.com
 Seq primer: T7
 High quality sequence stop: 346
 POLYA=No.

FEATURES source
 1..346
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="mRNA"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /tissue_type="heading leaf"
 /note="folding stage"
 /dev stage="folding stage"
 /lab host="E.coli DH10B(Zip)"
 /clone_lib="GIBCOBRL CAT. NO. 19643-014"
 /note="vector: pZLI; Site_1: NotI; Site_2: SalI; cDNA library was constructed by SUPERScriptTM Lambda System for cDNA Synthesis and Cloning (GIBCOBRL, CAT.NO.19643-014)"

ORIGIN

Alignment Scores:
 Pred. No.: 6.8e-25 Length: 346
 Score: 301.00 Matches: 50
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252a-10 (1-50) x CA992140 (1-346)

Qy 1 LysLeuCySGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 27 AAGTTGTCGAGAGTCAAGTGGGACATGTCAGGAGTCTGTGAAACAAATACGCCTGC 86
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 87 AAGATCATGTCATTCGACTTGAAGGAGCACACATGATGATGCACTATGTTCCCT 146
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 147 GCTCAAGTGTACTGTATTTCCTATGT 176

RESULT 2
 CD832294
 LOCUS CD832294 409 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN40.062L22F011227 BN40 Brassica napus cDNA clone BN40062L22, mRNA sequence.
 ACCESSION CD832294.1 GI:32514234
 VERSION CD832294.1
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 409)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES source

Location/Qualifiers
 1..409
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40062L22"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 7.75e-23 Length: 409
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252a-10 (1-50) x CD832294 (1-409)

Qy 1 LysLeuCySGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 141 AAGCTGTGCGAAGGCCAAGTGGACGTTGGTCAGGAGTCTGTGAAACAAATATGCATGC 200
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 201 AAGAATCAGTGCATTCGACTAGAGAAAGCACACATGATCTTGCACTATGTCTTCCCA 260
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 261 GCTCAAGTGTACTGTACTTCCCTGT 290

RESULT 3

CD834852
 LOCUS CD834852 425 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN45.043G08F011229 BN45 Brassica napus cDNA clone BN45043G08, mRNA sequence.
 ACCESSION CD834852
 VERSION CD834852.1 GI:32516792
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 425)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES source

Location/Qualifiers
 1..425
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45043G08"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:

Pred. No.: 8,186-23 Length: 425
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD834852 (1-425)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 139 AAGCTGTGCGAAGGCCAAGTGGACGTCGTGAGGAGTCGTGGAAACAATAATGCAATC 198
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 199 AAGATCAGTCATTCACATGAGAAAGCAGCATGATCTTGCACATATGCTTCCCA 258
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 259 GCTCACAAGTCATCTGCTACTTCCCTTGT 288

RESULT 4

CD833613
 LOCUS BN40.067P16F011228 BN40 mRNA linear EST 10-JUL-2003
 DEFINITION 427 bp Brassica napus cDNA clone BN40067P16, mRNA
 sequence.

ACCESSION CD833613

VERSION CD833613.1 GI:32515553

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

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Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

1..427
 /location=Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40067P16"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 8,236-23 Length: 427
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833613 (1-427)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 141 AAGCTGTGCGAAGGCCAAGTGGACGTCGTGAGGAGTCGTGGAAACAATAATGCAATC 200
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 201 AAGATCAGTGCATTCGACTAGAGAAAGCAGCATGGATCTTGCACATATGCTTCCCA 260
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 261 GCTCACAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 5

CD833047

LOCUS

DEFINITION BN40.065M05F011229 BN40 mRNA linear EST 10-JUL-2003
 sequence.

ACCESSION CD833047

VERSION CD833047.1 GI:32514987

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (Bases 1 to 449)

AUTHORS Genoplatte.

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

1..449
 /location=Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40065M05"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 8,826-23 Length: 449
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833047 (1-449)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 122 AAGCTGTGCGAAGGCCAAGTGGACGTCGTGAGGAGTCGTGGAAACAATAATGCAATC 181

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 182 AAGATCAGTCATTCGACTAGAGAAAGCAGCATGATCTTGCACATATGCTTCCCA 241

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 242 GCTCACAAGTGCATCTGCTACTTCCCTTGT 271

RESULT 6

CD831226

LOCUS

DEFINITION BN40.058J10F011019 BN40 mRNA linear EST 10-JUL-2003
 sequence.

ACCESSION CD831226

VERSION CD831226.1 GI:32513166

KEYWORDS EST.

SOURCE Brassica napus (rape)
ORGANISM

REFERENCE 1 (bases 1 to 457)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT

FEATURES
source
1. .457
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4008J10"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN

Alignment Scores:
Pred. No.: 9,048-23 Length: 457
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD831226 (1-457)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 141 AAGTTGTGTGAGAGCCCAAGTGGACATGTCAGGAGTTTGTGAAACAATAATGGTGT 200
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 201 AGAATCATGTCATTCGACTTGAAGAAGCAGCATGGAATCTTGCAACTATGTTCCCA 260
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 261 GCTCACAGTGTATCTGCTATTTCCCTGT 290

RESULT 7
CD834995

LOCUS CD834995 473 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.043008F011229 BN45 Brassica napus cDNA clone BN45043008, mRNA sequence.
ACCESSION CD834995
VERSION CD834995.1 GI:32516935
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM

REFERENCE 1 (bases 1 to 473)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT

Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES
source
1. .473
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45043008"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Alignment Scores:
Pred. No.: 9,498-23 Length: 473
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD834995 (1-473)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGTGAGAGCCCAAGTGGACATGTCAGGAGTTTGTGAAACAATAATGGTGT 218
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AGAATCATGTCATTCGACTTGAAGAAGCAGCATGGAATCTTGCAACTATGTTCCCA 278
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAGTGTATCTGCTATTTCCCTGT 308

RESULT 8
CD833784

LOCUS CD833784 476 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.001122F010914 BN45 Brassica napus cDNA clone BN45001122, mRNA sequence.
ACCESSION CD833784
VERSION CD833784.1 GI:32515724
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM

REFERENCE 1 (bases 1 to 476)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT

Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES
source
1. .476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45001122"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Alignment Scores:
Pred. No.: 9,576-23 Length: 476

Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833784 (1-476)

QY 1 LysLeuCysGluArgSerSerglyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 160 AAGTTGTGTGAGAGGCCAAGTGGACATGTCAGGAGTTGTGGAAACAATATGCGTGT 219
 |||||
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 220 AAGAATCAGTCATTCGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 279
 |||||
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||
 Db 280 GCTCAAGTGTATCTGCTATTTCCCTTGT 309
 |||||

RESULT 9
 CD834092
 LOCUS
 DEFINITION
 BN45.040I23F011018 BN45 Brassica napus cDNA clone BN45040I23, mRNA
 sequence.
 ACCESSION
 CD834092
 VERSION
 CD834092.1 GI:32516032
 KEYWORDS
 EST.
 SOURCE
 Brassica napus (rape)
 ORGANISM
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE
 1 (bases 1 to 476)
 AUTHORS
 Genoplatte, a major partnership french program in plant genomics
 TITLE
 Genoplatte, a major partnership french program in plant genomics
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).
 Location/Qualifiers
 1..476
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040I23"
 /tissue_type="seed"
 /clone_lib="BN45"

FEATURES

source
 1..476
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040I23"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:
 Pred. No.: 9.57e-23 Length: 476
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD834092 (1-476)

QY 1 LysLeuCysGluArgSerSerglyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 160 AAGTTGTGTGAGAGGCCAAGTGGACATGTCAGGAGTTGTGGAAACAATATGCGTGT 219
 |||||
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 220 AAGAATCAGTCATTCGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 279
 |||||

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||
 Db 280 GCTCAAGTGTATCTGCTATTTCCCTTGT 309
 |||||

RESULT 10

CD833924
 LOCUS
 DEFINITION
 BN45.040A03F011018 BN45 Brassica napus cDNA clone BN45040A03, mRNA
 sequence.
 ACCESSION
 CD833924
 VERSION
 CD833924.1 GI:32515864
 KEYWORDS
 EST.
 SOURCE
 Brassica napus (rape)
 ORGANISM
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE
 1 (bases 1 to 481)
 AUTHORS
 Genoplatte, a major partnership french program in plant genomics
 TITLE
 Genoplatte, a major partnership french program in plant genomics
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).
 Location/Qualifiers
 1..481
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040A03"
 /tissue_type="seed"
 /clone_lib="BN45"

FEATURES

source
 1..481
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040A03"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:
 Pred. No.: 9.71e-23 Length: 481
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833924 (1-481)

QY 1 LysLeuCysGluArgSerSerglyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 159 AAGTTGTGTGAGAGGCCAAGTGGACATGTCAGGAGTTGTGGAAACAATATGCGTGT 218
 |||||
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 219 AAGAATCAGTCATTCGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 278
 |||||

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||
 Db 279 GCTCAAGTGTATCTGCTATTTCCCTTGT 308
 |||||

RESULT 11

CD833627
 LOCUS
 DEFINITION
 BN45.001A11F010914 BN45 Brassica napus cDNA clone BN45001A11, mRNA
 sequence.
 ACCESSION
 CD833627
 VERSION
 CD833627.1 GI:32515567
 KEYWORDS
 EST.
 SOURCE
 Brassica napus (rape)
 ORGANISM
 Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 482)

Genoplaente, a major partnership french program in plant genomics

Genoplaente, unpublished (2003)

Contact: Genoplaente

Genoplaente

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplaente' (<http://www.genoplaente.com>

and <http://genoplaente-info.infobiogen.fr>).

FEATURES

source
1..482

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet neuf"

/db_xref="taxon:3708"

/clone="BN45001A11"

/tissue_type="seed"

/clone_lib="BN45"

ORIGIN

Alignment Scores:

Pred. No.: 9.74e-23 Length: 482
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833627 (1-482)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

DB 160 AAGTTGTGTGAGGCCNAGTGGACATGTCAGGAGTTTGTGGAACCAATATGCGTGT 219

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

DB 220 AAGATCATGTCATTCGACTTGAGAAAGCAGCATGATCTTGCAACTATGCTTCCCA 279

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

DB 280 GCTCACAAGTGTATCTGCTATTTCCCTTGT 309

RESULT 12

CD833661

LOCUS BN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA

DEFINITION 523 bp mRNA linear EST 10-JUL-2003

sequence.

ACCESSION CD833661

VERSION CD833661.1 GI:32515601

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 523)

Genoplaente, a major partnership french program in plant genomics

Genoplaente, unpublished (2003)

Contact: Genoplaente

Genoplaente

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Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplaente' (<http://www.genoplaente.com>

and <http://genoplaente-info.infobiogen.fr>).

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Alignment Scores:

Pred. No.: 1.15e-22 Length: 543
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1

FEATURES

source

1..523

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet neuf"

/db_xref="taxon:3708"

/clone="BN45001C04"

/tissue_type="seed"

/clone_lib="BN45"

ORIGIN

Alignment Scores:

Pred. No.: 1.09e-22 Length: 523
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833661 (1-523)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

DB 142 AAGCTGTGCGAAGGCCAAGTGGACGTGTGAGAGTCTGTGGAAACAATATGCGATGC 201

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

DB 202 AAGAATCAGTGCATTCGACTAGAGAAAGCAGCATGATCTTGCAACTATGCTTCCCA 261

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

DB 262 GCTCACAAGTGCATCTGCTACTTCCCTTGT 291

RESULT 13

CD828840

LOCUS BN40.040A23F011019 BN40 Brassica napus cDNA clone BN40040A23, mRNA

DEFINITION 543 bp mRNA linear EST 10-JUL-2003

sequence.

ACCESSION CD828840

VERSION CD828840.1 GI:32510780

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 543)

Genoplaente, a major partnership french program in plant genomics

Genoplaente, unpublished (2003)

Contact: Genoplaente

Genoplaente

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplaente' (<http://www.genoplaente.com>

and <http://genoplaente-info.infobiogen.fr>).

FEATURES

source

1..543

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet neuf"

/db_xref="taxon:3708"

/clone="BN40040A23"

/tissue_type="seed"

/clone_lib="BN40"

ORIGIN

Alignment Scores:

Pred. No.: 1.15e-22 Length: 543
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1

Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD829840 (1-543)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 DB 141 AAGCTGTGCGAAGGCAAGTGGACGTGTCAGAGTCTGTGGAAACATAATGATGC 200
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 DB 201 AAGATCAGTCGATTCGACTAGAGAAAGCAGACATGGATCTTGCAACTATGCTTTCCCA 260
 QY 41 AlahisLysCysIleCysTyrPheProCys 50
 DB 261 GCTCAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 14
 CD830628
 LOCUS CD830628 543 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN40.046D16F011221 BN40 Brassica napus cDNA clone BN40046D16, mRNA
 ACCESSION CD830628
 VERSION CD830628.1 GI:32512568
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 543)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES

source
 1..543
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40046D16"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 1156-22 Length: 543
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD830628 (1-543)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 DB 141 AAGCTGTGCGAAGGCAAGTGGACGTGTCAGAGTCTGTGGAAACATAATGATGC 200
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 DB 201 AAGATCAGTCGATTCGACTAGAGAAAGCAGACATGGATCTTGCAACTATGCTTTCCCA 260
 QY 41 AlahisLysCysIleCysTyrPheProCys 50

DB 261 GCTCAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 15

CD829429
 LOCUS CD829429 646 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN40.042B06F011226 BN40 Brassica napus cDNA clone BN40042B06, mRNA
 ACCESSION CD829429
 VERSION CD829429.1 GI:32511369
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 646)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 COMMENT Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES

source
 1..646
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40042B06"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 1466-22 Length: 646
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD829429 (1-646)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 DB 135 AAGCTGTGCGAAGGCAAGTGGACGTGTCAGAGTCTGTGGAAACATAATGATGC 194

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 DB 195 AAGATCAGTCGATTCGACTAGAGAAAGCAGCAGCATGGATCTTGCAACTATGCTTTCCCA 254

QY 41 AlahisLysCysIleCysTyrPheProCys 50
 DB 255 GCTCAAGTGCATCTGCTACTTCCCTTGT 284

Search completed: May 13, 2004, 12:18:04
 Job time : 2525 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:57:25 ; Search time 59.5 Seconds
(without alignments)
3931.922 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

Sequence: 1 gtttattatgcatggc.....caaaaaaaaaaaaaaaaaaaaa 414

Scoring table:

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Ygapop 10.0			0.5
Fgapop 6.0			7.0
Delop 6.0			Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool.p/US0006252/runat.11052004.141656.22777/app.query.fasta.1.583
-DB=A Geneseq 29Jan04 -QMT=fastan -SUFFIX=tag -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252.cgn.1.81 @runat.11052004.141656.22777 -ICPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 29Jan04.*

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2:	Geneseq1990s.*
3:	Geneseq2000s.*
4:	Geneseq2001s.*
5:	Geneseq2002s.*
6:	Geneseq2003as.*
7:	Geneseq2003bs.*
8:	Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	442	58.8	80	2 AAR33706	Aar33706 Antifunga
2	442	58.8	80	2 AAR57325	Aar57325 Antimicro
3	434	57.7	80	2 AAW19280	Aaw19280 Raphanus
4	434	57.7	80	2 AAW19617	Aaw19617 Radish an
5	433	57.6	80	2 AAR33708	Aar33708 Antifunga
6	433	57.6	80	2 AAR57327	Aar57327 Antimicro
7	432	57.4	80	7 ADC51222	Adc51222 Brassica
8	425	56.5	80	7 ADC51224	Adc51224 Brassica
9	423	56.2	80	3 AAY91117	Aay91117 Raphanus
10	418	55.6	187	3 AAY84072	Aay84072 Amino aci

11	417	55.5	80	4 AAB61792	Aab61792 Radish an
12	407	54.1	80	3 AAY57564	Aay57564 Wasabia j
13	407	54.1	80	5 ABP53725	Abp53725 Wasabia j
14	403	53.6	80	2 AAW40351	Aaw40351 A. thalia
15	403	53.6	80	2 AAW40346	Aaw40346 A. thalia
16	403	53.6	80	6 ABP81292	Abp81292 Arabidops
17	402	53.5	80	3 ABP57565	Abp57565 Wasabia j
18	402	53.5	80	5 ABP53726	Abp53726 Wasabia j
19	397	52.8	80	4 AAW40345	Aaw40345 A. thalia
20	397	52.8	80	4 AAB61794	Aab61794 Arabidops
21	395.5	52.7	79	2 AAW35560	Aaw35560 Alyssum s
22	359	47.7	607	3 AAG41694	Aag41694 Arabidops
23	309	41.1	51	2 AAW40349	Aaw40349 Radish Rs
24	309	41.1	51	2 AAY00738	Aay00738 Antifunga
25	309	41.1	51	4 AAB67417	Aab67417 Amino aci
26	309	41.1	51	4 AAB30220	Aab30220 Radish de
27	309	41.1	51	4 AAB49470	Aab49470 Radish an
28	309	41.1	51	4 AAB61793	Aab61793 White mus
29	307	40.8	149	3 AAY84060	Aay84060 Amino aci
30	304	40.4	50	4 AAE10625	Aae10625 Radish pl
31	304	40.4	51	2 AAW40347	Aaw40347 A. thalia
32	304	40.4	149	3 AAY70323	Aay70323 Dahlia me
33	304	40.4	149	3 AAY84058	Aay84058 Amino aci
34	302	40.2	51	2 AAW26372	Aaw26372 Radish an
35	302	40.2	51	2 AAW26374	Aaw26374 Radish an
36	301	40.0	51	2 AAW26371	Aaw26371 Radish an
37	301	40.0	157	3 AAY84066	Aay84066 Amino aci
38	301	40.0	360	3 AAY84067	Aay84067 Fusion pr
39	300	39.9	51	2 AAW19281	Aaw19281 Raphanus
40	300	39.9	51	2 AAW19616	Aaw19616 Radish an
41	300	39.9	51	2 AAW26375	Aaw26375 Radish an
42	300	39.9	51	2 AAY00737	Aay00737 Antifunga
43	300	39.9	51	4 AAB67416	Aab67416 Amino aci
44	300	39.9	51	4 AAB20221	Aab20221 Radish de
45	300	39.9	51	4 AAB49471	Aab49471 Radish an

ALIGNMENTS

RESULT 1
AAR33706
ID AAR33706 standard; protein; 80 AA.

AC AAR33706;
XX
XX
XX 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
XX Antifungal protein Rs-AFPI.
XX
XX Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
XX fungicide; bactericide; antibiotic; antifungal; gram positive;
XX plant disease resistance; low toxicity.
XX
XX Raphanus sativus.
XX
XX WO305153-A1.
XX
XX 18-MAR-1993.
XX
XX 27-AUG-1992; 92WO-GB001570.
XX
XX 29-AUG-1991; 91GB-00018523.
XX 13-FEB-1992; 92GB-00003038.
XX 25-JUN-1992; 92GB-00013526.
XX (ICIL) IMPERIAL CHEM IND PLC.
XX
XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
XX Vanderleyden J;
XX WPI, 1993-100978/12.

PT Bacterial proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX
 XX Disclosure; Fig 35; 110pp; English.
 XX
 XX This sequence is antifungal protein Rs-APF1 from *Raphanus sativus*. The
 CC exact source and isolation of the encoding DNA sequence is unclear from
 CC the specification. The protein is useful for combating fungi or bacteria
 CC eg gram positive bacteria and plant pathogenic fungi. It has moderate
 CC sensitivity to ions and an apparent low toxicity for cultured human
 CC cells. Plants transformed with the encoding DNA show increased disease
 CC resistance. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 80 AA;
 SQ

Alignment Scores:
 Pred. No.: 3,96e-40 Length: 80
 Score: 442.00 Matches: 80
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 58.78% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAR33706 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTTTGGCTGCT 75
 DB 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAa 20
 QY 76 TTCGAGCACCACAAATGGTGGAGCAGACAGAACTTGTGCGAAGGCCAAGTGGACATGG 135
 DB 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACGATGCAAGATCAGTGCATTAACTTGCAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGATCTTCAACTATGCTTCCAGCTCAGCAAGTGCATCTGCTACTTTCCTTGT 255
 DB 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 2

AAR57325
 ID AAR57325 standard; protein; 80 AA.
 XX
 XX AAR57325;
 XX
 XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX
 XX Antimicrobial Rs-APF1.
 XX
 XX Antimicrobial; Rs-APF1; symbiosis; disease-resistance; fungus-resistance;
 KW Clavibacter xyl subsp. cynodontis; Cxc; crop improvement; endophyte.
 XX
 XX *Raphanus sativus*.
 OS
 XX
 XX WO9416076-A1.
 PN
 XX
 XX 21-JUL-1994.
 PD
 XX
 XX 05-JAN-1994; 94WO-GB000012.
 PF
 XX
 XX 08-JAN-1993; 93GB-00000281.
 FR
 XX
 XX (ZENE) ZENECA LTD.
 PA
 XX
 XX Dubock AC, Powell KA, Rees SB;
 PI
 XX
 XX WPI; 1994-249223/30.
 DR
 XX
 XX N-PSDB; AAQ70128.
 DR
 XX

PT Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 XX
 XX Disclosure; Page 32; 39pp; English.
 XX
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyl subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APF1 from *R. sativus*. The full-length cDNA
 CC sequence of Rs-APF1 is given in AAQ70128, and the amino acid sequence
 CC predicted from this sequence in AAR57325. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 XX Sequence 80 AA;
 SQ

Alignment Scores:
 Pred. No.: 3,96e-40 Length: 80
 Score: 442.00 Matches: 80
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 58.78% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAR57325 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTTTGGCTGCT 75
 DB 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAa 20
 QY 76 TTCGAGCACCACAAATGGTGGAGCAGACAGAACTTGTGCGAAGGCCAAGTGGACATGG 135
 DB 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACGATGCAAGATCAGTGCATTAACTTGCAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGATCTTCAACTATGCTTCCAGCTCAGCAAGTGCATCTGCTACTTTCCTTGT 255
 DB 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3

AAR19280
 ID AAR19280 standard; protein; 80 AA.
 XX
 XX AAR19280;
 XX
 XX 25-MAR-2003 (revised)
 DT 19-JAN-1998 (first entry)
 XX
 XX *Raphanus sativus* antifungal protein 1 (Rs-APF1).
 DE
 XX
 XX Antifungal protein; candida; fungal resistance; food additive; radish;
 KW crop protection; plant defensin; bacterial protection; preservative.
 XX
 XX *Raphanus sativus*.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..29
 FT Protein 13..80
 FT /label= antifungal_protein_1
 FT Misc-difference 24
 FT /note= "encoded by CCA"
 XX
 XX WO9721815-A2.
 FN
 XX
 XX 19-JUN-1997.
 PD
 XX
 XX 12-DEC-1996; 96WO-GB003068.
 PF
 XX
 XX 13-DEC-1995; 95GB-00025455.
 PR
 XX
 XX 28-MAR-1996; 96GB-00006552.
 PR

XX PA (ZENE) ZENECA LTD.
 XX FT Meloen RH, Puijk WC, Schaaper WMW, Sijtsma L, Van Amerongen A;
 PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
 XX FT Van Gelder WMJ;
 XX FT WPI; 1997-332786/30.
 DR N-PSDB; AAT72333.
 XX FT
 XX FT Antifungal peptide derived from radish antifungal protein 2 - and related
 PT DNA, useful for producing plants with increased fungal resistance and as
 PT therapeutic or preservative agent.
 XX FT
 XX PS Claim 1; Fig 2; 65pp; English.
 XX FT
 CC This protein sequence is a Raphanus sativus (radish) antifungal protein
 CC (RS-AFP1). Analogues of the homologous protein, RS-AFP2 (AAW19281), have
 CC also been produced (see AAW19282-92, AAW19294-98, AAW19301-04, AAW19330-
 CC 34 and AAW1765-83). Plants containing DNA sequences encoding these
 CC proteins have improved resistance to fungi. Compositions containing the
 CC peptides can be used to control fungi or bacteria in pharmaceutical (e.g.
 CC treatment of Candida infections) or preservative purposes (as food
 CC additives). In agriculture, the peptide may be used to improve disease
 CC resistance or disease tolerance of crops, either pre or post harvest.
 CC When applied to plants they may also have curative as well as protective
 CC actions. The peptides may also be used to protect plants by introducing
 CC them, or a microorganism capable of expressing the peptide into the soil.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX FT
 XX SQ Sequence 80 AA;

Alignment Scores:
 Pred. No.: 3,05e-39 Length: 80
 Score: 434.00 Matches: 79
 Percent Similarity: 98.75% Conservative: 0
 Best Local Similarity: 98.75% Mismatches: 1
 Query Match: 57.71% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAW19280 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTGTCTTTTGTGCTGT 75
 DB 1 MetAlalysPheAlaSerlleAlaLeuPheAlaLeuValLeuPheAlaLa 20
 QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGAGTTGTGGAAAGGCCAAGTGGGACATGG 135
 DB 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAAGTGCATTAACTTGAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTGTTGT 255
 DB 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 4
 AAW19617
 ID AAW19617 standard; protein; 80 AA.
 XX
 AC AAW19617;
 XX
 DT 13-DEC-1997 (first entry)
 XX
 DE Radish antifungal protein 1 (RS-AFP1).

KW RS-AFP1; radish antifungal protein 1; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX
 OS Raphanus sativus.
 XX

FT Key Location/Qualifiers
 FT Peptide 1..29
 FT /label= Pro-peptide
 FT Misc-difference 24
 FT /note= "encoded by CCA"
 FT Protein 30..80
 FT /label= Mat protein
 FT /note= "RsAFP1"
 XX
 XX WO9721814-A1.
 XX 19-JUN-1997.
 XX
 XX 12-DEC-1996; 96WO-GB003065.
 XX
 XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 XX Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 XX N-PSDB; AAT68696.
 XX
 XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX
 XX Disclosure; Fig 2; 39pp; English.

CC This polypeptide comprises the preprotein for radish antifungal protein 1
 CC (RS-AFP1). Novel antifungal proteins are based on RS-AFP1, RS-AFP2 (see
 CC AAW19616), RS-AFP3 and RS-AFP4, especially those in which Gly9 is replaced
 CC by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met.
 CC Mutants (see AAW26371-90) of RS-AFP2 are specifically claimed. The
 CC mutants show improved salt tolerant antifungal activity, particularly
 CC when expressed in plants

SQ Sequence 80 AA;

Alignment Scores:
 Pred. No.: 3,05e-39 Length: 80
 Score: 434.00 Matches: 79
 Percent Similarity: 98.75% Conservative: 0
 Best Local Similarity: 98.75% Mismatches: 1
 Query Match: 57.71% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAW19617 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTGTCTTTTGTGCTGT 75
 DB 1 MetAlalysPheAlaSerlleAlaLeuPheAlaLeuValLeuPheAlaLa 20
 QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGAGTTGTGGAAAGGCCAAGTGGGACATGG 135
 DB 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAAGTGCATTAACTTGAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTGTTGT 255
 DB 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 5
 AAW19617
 ID AAW19617 standard; protein; 80 AA.
 XX
 AC AAW19617;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-JUL-1993 (first entry)

XX Antifungal protein Rs-APP2.
 DE Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 XX fungicide; bactericide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX Raphanus sativus.
 OS WO9305153-A1.
 XX 18-MAR-1993.
 XX 27-AUG-1992; 92WO-GB001570.
 XX 29-AUG-1991; 91GB-00018523.
 XX 13-FEB-1992; 92GB-0003038.
 XX 25-JUN-1992; 92GB-00013526.
 XX (ICIL) IMPERIAL CHEM IND PLC.
 XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX WPI; 1993-100978/12.
 XX Biotic proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX Disclosure; Fig 35; 110pp; English.
 XX This sequence is part of antifungal protein Rs-APP2, decoded from a
 CC mutagenised RsAPP1 clone derived from Raphanus sativus. The protein is
 CC useful for combating fungi or bacteria eg gram positive bacteria and
 CC plant pathogenic fungi. It has moderate sensitivity to ions and an
 CC apparent low toxicity for cultured human cells. Plants transformed with
 CC the encoding DNA show increased disease resistance. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 80 AA;
 SQ
 Alignment Scores:
 Pred. No.: 3,93e-39 Length: 80
 Score: 433.00 Matches: 78
 Percent Similarity: 98.75% Conservative: 1
 Best Local Similarity: 97.50% Mismatches: 1
 Query Match: 57.58% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-19 (1-414) x AAR33708 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGTCTCTTTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCAACAAATGTGTGAAGCACAGAAAGTGTGCGAAGGCCCAAGTGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACGCAATCAGTGCATTAACTTGAGGAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
 QY 196 CGACATGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGTATCTGCTACTTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTy-ValPheProAlaHisLysCysIleCysTyrrPheProCys 80
 RESULT 6
 AAR57327
 ID AAR57327 standard; protein; 80 AA.
 XX AAR57327;
 AC

XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX Antimicrobial Rs-APP2.
 DE Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
 XX Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis.
 XX Raphanus sativus.
 OS WO9416076-A1.
 XX 21-JUL-1994.
 XX 05-JAN-1994; 94WO-GB000012.
 XX 08-JAN-1993; 93GB-00000281.
 XX (ZENE) ZENECA LTD.
 XX Dubock AC, Powell KA, Rees SB;
 PI WPI; 1994-249223/30.
 XX N-PSDB; AAQ70130.
 XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 XX Disclosure; Page 33-34; 39pp; English.
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APP1 from R. sativus. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX Sequence 80 AA;
 SQ
 Alignment Scores:
 Pred. No.: 3,93e-39 Length: 80
 Score: 433.00 Matches: 78
 Percent Similarity: 98.75% Conservative: 1
 Best Local Similarity: 97.50% Mismatches: 1
 Query Match: 57.58% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-19 (1-414) x AAR57327 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGTCTCTTTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCAACAAATGTGTGAAGCACAGAAAGTGTGCGAAGGCCCAAGTGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACGCAATCAGTGCATTAACTTGAGGAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
 QY 196 CGACATGATCTTGCACACTATGTCTTCCAGCTCACAAAGTGTATCTGCTACTTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTy-ValPheProAlaHisLysCysIleCysTyrrPheProCys 80
 RESULT 7
 ADCS1222
 ID ADCS1222 standard; protein; 80 AA.
 XX

AC ADC51222;
 XX DT 18-DEC-2003 (first entry)
 XX DE Brassica oleracea defensin protein.
 XX DE antimicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight.
 XX OS Brassica oleracea.
 XX PN JP2003088379-A.
 XX PD 25-MAR-2003.
 XX PF 18-SEP-2001; 2001JP-00283117.
 XX PR 18-SEP-2001; 2001JP-00283117.
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX DR N-PSDB; ADC51221.
 XX PT Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.
 XX PS Claim 1; SEQ ID NO 2; 34pp; Japanese.
 XX CC The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present amino acid sequence
 CC represents a Brassica defensin protein of the invention.
 XX SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 5.07e-39 Length: 80
 Score: 432.00 Matches: 78
 Percent Similarity: 97.50% Conservative: 0
 Best Local Similarity: 97.50% Mismatches: 2
 Query Match: 57.45% Indels: 0
 DB: 7 Gaps: 0
 US-10-006-252A-19 (1-414) x ADC51222 (1-80)
 QY 16 ATGGCTAAGTTGGCTCCATCGCACTTCTTTTGGCTGCTGCTTTTGGCTGCT 75
 Db 1 MetAlaLysPheValSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
 QY 76 TTGAGACCAACAACTGGTGGAGCAGAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
 Db 21 LeuGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAACTACGATCGAAGATCACTGATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
 RESULT 8
 ADC51224

ID ADC51224 standard; protein; 80 AA.
 XX AC ADC51224;
 XX DT 18-DEC-2003 (first entry)
 XX DE Brassica defensin protein.
 XX DE antimicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight.
 XX OS Brassica sp.
 XX PN JP2003088379-A.
 XX PD 25-MAR-2003.
 XX PF 18-SEP-2001; 2001JP-00283117.
 XX PR 18-SEP-2001; 2001JP-00283117.
 XX PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX DR WPI; 2003-621123/59.
 XX DR N-PSDB; ADC51223.
 XX PT Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.
 XX PS Claim 1; SEQ ID NO 4; 34pp; Japanese.
 XX CC The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present amino acid sequence
 CC represents a Brassica defensin protein of the invention.
 XX SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 3.02e-38 Length: 80
 Score: 425.00 Matches: 77
 Percent Similarity: 96.25% Conservative: 0
 Best Local Similarity: 96.25% Mismatches: 3
 Query Match: 56.52% Indels: 0
 DB: 7 Gaps: 0
 US-10-006-252A-19 (1-414) x ADC51224 (1-80)
 QY 16 ATGGCTAAGTTGGCTCCATCGCACTTCTTTTGGCTGCTGCTTTTGGCTGCT 75
 Db 1 MetAlaLysPheValSerIleIleAlaLeuPheAlaAlaLeuValLeuAlaAla 20
 QY 76 TTGAGACCAACAACTGGTGGAGCAGAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAACTACGATCGAAGATCACTGATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 9
 AAY91117
 ID AAY91117 standard; protein; 80 AA.
 XX
 AC AAY91117;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Raphanus sativus antibacterial protein radishin SEQ ID NO:2.
 XX
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
 KW pathogenic microbe; radish; rice blast disease.
 XX
 OS Raphanus sativus.
 XX
 PN JP2000116379-A.
 XX
 PD 25-APR-2000.
 XX
 PF 09-OCT-1998; 98JP-00288472.
 XX
 PR 09-OCT-1998; 98JP-00288472.
 XX
 PA (TOYA-) TOYAMA KEN.
 XX
 DR WPI: 2000-389821/34.
 DR N-PSDB; AAA53190.
 XX
 PT Isolated DNA from Raphanus sativus used to transform a microbe and a
 PT plant to produce an antibacterial protein used to increase resistance of
 PT rice paddy against pathogenic microbes.
 XX
 PS Claim 5; Page 4-5; 7pp; Japanese.
 XX
 CC The present sequence represents an antibacterial protein, designated
 CC radishin, isolated from Raphanus sativus (radish). A phage or plasmid
 CC comprising radishin can be used for increasing resistance of paddy and
 CC rice blast disease against pathogenic microbes
 XX
 SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 5,04e-38 Length: 80
 Score: 423.00 Matches: 75
 Percent Similarity: 97.50% Conservative: 3
 Best Local Similarity: 93.75% Mismatches: 2
 Query Match: 56.25% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-19 (1-414) x AAY91117 (1-80)
 Qy 16 ATGGCTAAGTTGGCTGCATATCGCACTTTCTTTGCTGCTCTTTGCTTTGCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleValLeuLeuPheAlaLeuValPheSerAla 20
 Qy 76 TTCGAAGCACCACCAATGTGTGAAGCACAGAGTTGTGCAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 Qy 136 TCAGGAGTCTGTGGAAACAAATAACCCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
 Qy 196 CGACATGGATCTTGCAACTATGCTCTCCAGCTCACAAAGTGTATCTGCTACTTTCCTGCT 255
 Db 61 ArgHisGlySerCysAsnTyValPheProAlaHisLysCysIleCysTyPheProCys 80
 RESULT 10
 AAY84072
 ID AAY84072 standard; protein; 187 AA.
 XX
 AC AAY84072;
 XX
 XX

DT 03-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of a fusion protein of DmAMP1 and RsAPP2.
 XX
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2.
 XX
 OS Synthetic.
 OS Dahlia merckii.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Protein 29..78
 FT Peptide /note= "DmAMP1"
 FT Peptide 79..136
 FT Protein /note= "linker"
 FT Protein 137..187
 FT Protein /note= "RsAPP2"
 XX
 PN WO200011175-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 17-AUG-1999; 99WO-GB002716.
 XX
 PR 18-AUG-1998; 98GB-00018001.
 PR 04-DEC-1998; 98GB-00026753.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Broekaert WF, Francois IEUA, De Bolle MFC, Evans IJ, Ray JA;
 XX
 DR WPI: 2000-246564/21.
 DR N-PSDB; AA299339.
 XX
 CC Improving expression of polyproteins in plants involves coexpression of
 CC two or more proteins in plants within a single transcription unit.
 XX
 PS Claim 33; Fig 34; 151pp; English.
 XX
 CC The present sequence represents a protein of the invention, comprising
 CC the mature proteins of the plant defensins, the Dahlia antimicrobial
 CC protein (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker
 CC propeptide of the invention. The specification describes methods for
 CC improving expression levels of one or more proteins in a transgenic
 CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 CC comprising a cleavage site, whereby the expressed polypeptide is post-
 CC translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptidic sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence
 XX
 SQ Sequence 187 AA;
 Alignment Scores:
 Pred. No.: 2.17e-37 Length: 187
 Score: 418.00 Matches: 76
 Percent Similarity: 96.25% Conservative: 1
 Best Local Similarity: 95.00% Mismatches: 3
 Query Match: 55.59% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-19 (1-414) x AAY84072 (1-187)
 Qy 16 ATGGCTAAGTTGGCTGCATATCGCACTTTCTTTGCTGCTCTTTGCTTTGCTGCT 75
 Db 108 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValPheAlaAla 127
 Qy 76 TTCGAAGCACCACCAATGTGTGAAGCACAGAGTTGTGCAAGGCCAAGTGGGACATGG 135

Db 128 PheGluAlaProThrWetValGluAlaGlnLysLeuCysGlnArgProSerArgThrTrp 147
 QY 136 TCAGGAGTCTGGGAACATTAACCATGCGAAGATCATGTCATTAACCTTGAGAAAGCA 195
 Db 148 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAaGLeuGluLysAla 167
 QY 196 CGACATGGAATCTGCAATATGCTCTTCCAGCTCACAAGTGTATCTCTACTTCTCTGT 255
 Db 168 ArgHisGlySerCysAsnTyArgPheProAlaHisLysCysIleCysTyrPheProCys 187

RESULT 11
 AAB61792
 ID AAB61792 standard; protein; 80 AA.
 AC AAB61792;
 XX
 XX 20-APR-2001 (first entry)
 XX Radish antifungal defensin.
 DE
 DE Radish antifungal defensin.
 KW Sunflower; anti-pathogenic; pathogenesis-related protein-5; PR5; BBE;
 KW defensin; berberine bridge enzyme; plant pathogen; disease resistance;
 KW agricultural; pharmaceutical; antifungal; antibacterial; antiviral;
 KW antimicrobial; gene therapy; radish.
 XX
 OS Raphanus sativus.
 OS
 XX
 XX WO200078983-A2.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-US017090.
 XX
 XX 23-JUN-1999; 99US-0140646P.
 PR 01-NOV-1999; 99US-0162904P.
 PR 08-JUN-2000; 2000US-00589733.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Bidney DL, Crasta OR, Duvick JP, Hu X, Lu G;
 XX WPI; 2001-102729/11.
 XX
 XX Increasing pathogen (e.g. fungus, bacteria and virus) resistance in
 PT plants, comprises transforming plants with a DNA construct containing a
 PT nucleic acid sequence encoding anti-pathogenic proteins.
 XX
 XX Disclosure; Fig 4; 86pp; English.
 XX

The invention relates to sunflower anti-pathogenic proteins such as pathogenesis-related protein-5 (PR5), defensin and berberine bridge enzyme (BBE). DNA constructs containing nucleotide sequences encoding the anti-pathogenic proteins are useful for increasing resistance against pathogens e.g. fungal pathogen in monocot or dicot plants. The purified sunflower proteins (PR5, defensin or BBE) and compositions containing the proteins are useful for controlling plant pathogen by using procedures of spraying, dusting, scattering or seed coating, to the plants or the environment of the pathogen. The anti-pathogenic genes are useful as genetic markers in disease resistance breeding programs. Promoters capable of driving expression of the proteins are useful to express anti-pathogenic genes including disease and insect resistance genes. The proteins can also be used in agricultural and pharmaceutical compositions as antifungal and antimicrobial agents. The nucleotide sequences encoding the anti-pathogenic proteins are useful for transgenic plant production and for enhancing plant defense mechanism. The present sequence represents a radish antifungal defensin (Swiss-Prot Accn No. P30230), used in homology studies with sunflower defensin

XX Sequence 80 AA;
 SQ

Alignment Scores:
 Pred. No.: 2.33e-37 Length: 80
 Score: 407.00 Matches: 80
 Percent Similarity: 96.25% Conservativeness: 72
 Best Local Similarity: 90.00% Mismatches: 3
 Query Match: 54.12% Indels: 0
 DB: Gaps: 0

Score: 417.00 Matches: 74
 Percent Similarity: 95.00% Conservativeness: 2
 Best Local Similarity: 92.50% Mismatches: 4
 Query Match: 55.45% Indels: 0
 DB: Gaps: 0

US-10-006-252A-19 (1-414) x AAB61792 (1-80)
 QY 16 ATGGCTAAGTTGGCTGCATCATCGCACTTCTTTTGGCTCTCTGTTCTTTTGGCTGT 75
 Db 1 MetAlaLysPheAlaSerIleIleValLeuLeuPheValAlaLeuValPheAlaAla 20
 QY 76 TTCGAGCACCACAAATGGTGGAGACACAGAGTTGTGCAAGGCCAAAGTGGGACATGG 135
 Db 21 PheGluGluProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGAAAACAATAACGCATGCAAGAATCAGTCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
 QY 196 CGACATGGAATCTTCCAACTATGCTTCCAGCTCACAAGTGTATCTCTACTTCTCTGT 255
 Db 61 ArgHisGlySerCysAsnTyValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 12
 AAY57564
 ID AAY57564 standard; protein; 80 AA.
 XX
 AC AAY57564;
 XX
 XX 12-SEP-2003 (revised)
 DT 01-MAR-2000 (first entry)
 XX
 XX Wasabia japonica antibacterial protein SEQ ID NO:2.
 DE Wasabia japonica; antibacterial; food additive.
 KW Wasabia japonica; antibacterial; food additive.
 XX
 OS Eutrema wasabi.
 OS
 XX JP11313678-A.
 XX
 XX 16-NOV-1999.
 XX
 XX 30-APR-1998; 98JP-00121303.
 PF
 XX 30-APR-1998; 98JP-00121303.
 PR
 XX (IWAT-) IWATE KEN.
 XX
 XX WPI; 2000-057353/05.
 DR
 DR N-PSDB; AAZ39123.
 XX
 XX An antibacterial protein gene of Wasabia japonica - useful as a food- or
 PT feed-additive.
 XX
 XX Claim 1; Page 13; 16pp; Japanese.
 PS
 XX The present sequence represents an antibacterial protein isolated from
 CC Wasabia japonica. The antibacterial protein can be used as a food or feed
 CC additive. (Updated on 12-SEP-2003 to standardise OS field)
 CC
 XX Sequence 80 AA;
 SQ

Alignment Scores:
 Pred. No.: 2.98e-36 Length: 80
 Score: 407.00 Matches: 72
 Percent Similarity: 96.25% Conservativeness: 5
 Best Local Similarity: 90.00% Mismatches: 3
 Query Match: 54.12% Indels: 0
 DB: Gaps: 0

US-10-006-252A-19 (1-414) x AAY57564 (1-80)

QY 16 ATGGCTAAGTTGCGTCCATCATCCGACCTCTTTTGTCTGCTCTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheSerAla 20
 QY 76 TTCGAAGCACCAACAAATGCTGGAAGCACAGAAAGTTGTGCGAAAGGCCAACAGTGGGACATGG 135
 Db 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATACGATGCAAGATCAGTGCATTACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAGTGTATCTGCTACTTCTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysIlePheProCys 80
 RESULT 13
 ID ABP53725 standard; protein; 80 AA.
 AC ABP53725;
 XX
 DT 02-JAN-2003 (first entry)
 DE Wasabia japonica gamma-thionin protein SEQ ID NO:2.
 XX Wasabia japonica; gamma-thionin; plant; disease-resistant plant.
 XX Eutrema wasabi.
 XX JP200272292-A.
 XX 24-SEP-2002.
 XX 22-MAR-2001; 2001JP-00083526.
 XX 22-MAR-2001; 2001JP-00083526.
 XX (IWAT-) IWATE KEN.
 XX WPI; 2002-718704/78.
 DR N-PSDB; ABQ82690.
 XX A disease-resistant plant in which wasabi gamma-thionin gene is
 PT introduced, creation of the disease-resistant plant.
 XX
 PS Claim 2; Page 8; 11pp; Japanese.
 CC The present invention describes a disease-resistant plant in which a
 CC wasabi gamma-thionin gene is introduced. Also described is a method for
 CC the creation of the above disease-resistant plant by introducing a wasabi
 CC gamma-thionin gene to a plant. The present sequence represents a Eutrema
 CC wasabi (Wasabia japonica) gamma-thionin protein from the present
 CC invention
 XX
 SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 2,98e-36 Length: 80
 Score: 407.00 Matches: 72
 Percent Similarity: 95.25% Conservative: 5
 Best Local Similarity: 90.00% Mismatches: 3
 Query Match: 54.12% Indels: 0
 DB: 5 Gaps: 0
 US-10-006-252A-19 (1-414) x ABP53725 (1-80)
 QY 16 ATGGCTAAGTTGCGTCCATCATCCGACCTCTTTTGTCTGCTCTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheSerAla 20
 QY 76 TTCGAAGCACCAACAAATGCTGGAAGCACAGAAAGTTGTGCGAAAGGCCAACAGTGGGACATGG 135
 Db 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40

Db 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATACGATGCAAGATCAGTGCATTACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAGTGTATCTGCTACTTCTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysIlePheProCys 80
 RESULT 14
 ID AAW40351 standard; protein; 80 AA.
 AC AAW40351;
 XX
 DT 23-JUN-1998 (first entry)
 DE A. thaliana PDF1.2 protein.
 XX
 KW Defensein; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
 XX fungi.
 OS Arabidopsis thaliana.
 XX
 FN WO9800023-A2.
 PD 08-JAN-1998.
 XX
 XX 20-JUN-1997; 97WO-CB001672.
 XX
 PR 01-JUL-1996; 96GB-00013753.
 XX
 XX (ZENE) ZENECA LTD.
 XX
 XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
 PI Kazan K;
 XX
 DR WPI; 1998-086663/08.
 DR N-PSDB; AAV10646.
 XX
 PT Protecting plants against pathogens by inducing defensin genes - by
 PT stimulating ethylene or jasmonate pathways, also new promoter of defensin
 PT gene from Arabidopsis.
 XX
 PS Claim 20; Fig 14; 72pp; English.
 CC This sequence represents an Arabidopsis PDF1.2 gene which is used in a
 CC novel method for the protection of plants against pathogens which
 CC involves inducing expression of a plant defensin gene by stimulating the
 CC jasmonate and/or ethylene pathways. The method is used to induce
 CC protection against necrotrophic pathogens, specifically fungi and does
 CC not require cytotoxic or potentially harmful chemicals
 XX
 SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 8,26e-36 Length: 80
 Score: 403.00 Matches: 71
 Percent Similarity: 95.00% Conservative: 5
 Best Local Similarity: 88.75% Mismatches: 4
 Query Match: 53.59% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-19 (1-414) x AAW40351 (1-80)
 QY 16 ATGGCTAAGTTGCGTCCATCATCCGACCTCTTTTGTCTGCTCTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheAla 20
 QY 76 TTCGAAGCACCAACAAATGCTGGAAGCACAGAAAGTTGTGCGAAAGGCCAACAGTGGGACATGG 135
 Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATTAAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCAGTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 15

AAW40346

ID AAW40346 standard; protein; 80 AA.

AC AAW40346;

DT 23-JUN-1998 (first entry)

DE A. thaliana PDF1.2 protein.

KW Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene; fungi.

OS Arabidopsis thaliana.

FX Key Location/Qualifiers

FT Peptide 1..29

FT Protein /label= signal

FT /label= PFD1.2

FT /note= "plant defensin"

PN WO9800023-A2.

PD 08-JAN-1998.

PF 20-JUN-1997; 97WO-GB001672.

PR 01-JUL-1996; 96GB-00013753.

PA (ZENE) ZENECA LTD.

PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM; Kazan K;

DR WPI; 1998-086663/08.

XX N-PSDB; AAV10633.

PT Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.

PS Disclosure; Fig 1; 72pp; English.

CC This sequence represents the Arabidopsis PDF1.2 protein which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals

SQ Sequence 80 AA;

Alignment Scores:

Pred. No.:	8.26e-36	Length:	80
Score:	403.00	Matches:	71
Percent Similarity:	95.00%	Conservative:	5
Best Local Similarity:	88.75%	Mismatches:	4
Query Match:	53.59%	Indels:	0
DB:	2	Gaps:	0

US-10-006-252A-19 (1-414) x AAW40346 (1-80)

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Db 1 MetalAlaLysPheAlaSerIleIleThrLeuIlePheAlaAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAGACCAACAATGGTGGAGACACAGAAGTTGTGCCAAGGCCCAAGTGGGACATGG 135
 Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATTAAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCAGTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

Search completed: May 11, 2004, 17:02:15
 Job time : 62.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 17:00:09 ; Search time 22 Seconds
(without alignments)
1943.014 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

Sequence: 1 gttttattagtcattggc.....caaaaaaaaaaaaaaaaaaa 414

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -NORM=ext -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pcp.*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pcp.*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pcp.*
- 5: /cgn2_6/prodata/2/iaa/6CTUS COMB.pcp.*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	58.8	80	1	US-08-377-687-49
2	442	58.8	80	2	US-08-777-192-49
3	442	58.8	80	3	US-08-971-982-49
4	434	57.7	80	3	US-09-103-489-20
5	434	57.7	80	4	US-09-829-381D-20
6	433	57.6	80	1	US-08-377-687-59
7	433	57.6	80	2	US-08-777-192-59
8	433	57.6	80	3	US-08-971-982-59
9	417	55.5	80	4	US-09-589-733C-21
10	397	52.8	80	4	US-09-589-733C-23
11	396.5	52.7	79	1	US-08-627-706-15
12	396.5	52.7	79	3	US-09-103-489-15

13	396.5	52.7	79	4	US-09-829-381D-15
14	309	41.1	51	1	US-08-377-687-19
15	309	41.1	51	1	US-08-627-706-18
16	309	41.1	51	2	US-08-777-192-19
17	309	41.1	51	3	US-08-971-982-19
18	309	41.1	51	3	US-09-103-489-18
19	309	41.1	51	4	US-09-077-951-8
20	309	41.1	51	4	US-09-077-948A-34
21	309	41.1	51	4	US-09-829-381D-18
22	309	41.1	51	4	US-09-589-733C-22
23	307	40.8	51	1	US-08-656-318A-3
24	307	40.8	51	2	US-08-956-459-3
25	302	40.2	51	4	US-09-077-951-58
26	302	40.2	51	4	US-09-077-951-60
27	301	40.0	51	4	US-09-077-951-57
28	300	39.9	51	1	US-08-627-706-19
29	300	39.9	51	3	US-09-103-489-19
30	300	39.9	51	4	US-09-077-951-9
31	300	39.9	51	4	US-09-077-951-20
32	300	39.9	51	4	US-09-077-951-61
33	300	39.9	51	4	US-09-077-948A-35
34	300	39.9	51	4	US-09-829-381D-19
35	298	39.6	51	1	US-08-656-318A-4
36	298	39.6	51	2	US-08-956-459-4
37	296	39.4	51	4	US-09-077-951-22
38	296	39.4	51	4	US-09-077-951-29
39	296	39.4	51	4	US-09-077-951-65
40	295	39.2	51	4	US-09-077-951-31
41	295	39.2	51	4	US-09-077-951-39
42	295	39.2	51	4	US-09-077-951-44
43	295	39.2	51	4	US-09-077-951-77
44	294	39.1	51	4	US-09-077-951-28
45	294	39.1	51	4	US-09-077-951-41

ALIGNMENTS

RESULT 1

US-08-377-687-49
; Sequence 49, Application US/08377687
; Patent No. 5338525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCES/DOCKET NUMBER: 93042/SER.36525/US/A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-377-687-49

Alignment Scores:
Pred. No.: 5,13e-45 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 1 Gaps: 0

US-10-006-252a-19 (1-414) x US-08-377-687-49 (1-80)

Qy 16 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTCTTTTGTGCTGT 75
Db 1 MetAlaLysPheAlaSerIlelleAlaLeuPheAlaLeuValLeuPheAlaLa 20
Qy 76 TTCGAGCACCACAAATGGTGGAGCACAGAGTTGTGGAAAGGCGAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Qy 136 TCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Qy 196 CGACATGATCTTGAACATGTCTTCCAGCTCACAAGTATCTGCTACTTCTGCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 2

US-08-777-192-49
Sequence 49, Application US/08777192
Patent No. 5824869

GENERAL INFORMATION:

APPLICANT: BROEKART, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-777-192-49

Alignment Scores:
Pred. No.: 5,13e-45 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 2 Gaps: 0

US-10-006-252a-19 (1-414) x US-08-777-192-49 (1-80)

Qy 16 ATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTCTTTTGTGCTGT 75
Db 1 MetAlaLysPheAlaSerIlelleAlaLeuPheAlaLeuValLeuPheAlaLa 20
Qy 76 TTCGAGCACCACAAATGGTGGAGCACAGAGTTGTGGAAAGGCGAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Qy 136 TCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Qy 196 CGACATGATCTTGAACATGTCTTCCAGCTCACAAGTATCTGCTACTTCTGCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3

US-08-971-982-49
Sequence 49, Application US/08971982
Patent No. 6187904

GENERAL INFORMATION:

APPLICANT: BROEKART, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF

TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-No. 6187904-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 49:

US-08-971-982-49

Alignment Scores:

Pred. No.: 5,13e-45 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.78% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-19 (1-414) x US-08-971-982-49 (1-80)

QY 16 ATGGCTAAGTTGGCTCCATCATCGCACTCTTTTGTCTCTCTTTTGTCTCTCTTTTGTCTCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaValLeuPheAlaAla 20
QY 76 TTCGAGCACCACCAATGCTGGAGACACAGAGTTGCGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCySGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGAAACAATAACGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGATCTTGCACATATGTTCCAGCTCACAAGTGTATCTGCTACTTCTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrrValPheProAlaHisLysCysIleCysTyrrPheProCys 80

RESULT 4

US-09-103-489-20

Sequence 20, Application US/09103489

Patent No. 6215048

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yennie S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

CONTROLLING PLANT PATHOGENIC FUNGI

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/103,489

FILING DATE: 24-JUN-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-103-489-20

Alignment Scores:

Pred. No.: 4,74e-44 Length: 80
Score: 434.00 Matches: 79
Percent Similarity: 98.75% Conservative: 0
Best Local Similarity: 98.75% Mismatches: 1
Query Match: 57.71% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-103-489-20 (1-80)

QY 16 ATGGCTAAGTTGGCTCCATCATCGCACTCTTTTGTCTCTCTTTTGTCTCTCTTTTGTCTCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaValLeuPheAlaAla 20
QY 76 TTCGAGCACCACCAATGCTGGAGACACAGAGTTGCGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCySGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGAAACAATAACGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGATCTTGCACATATGTTCCAGCTCACAAGTGTATCTGCTACTTCTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrrValPheProAlaHisLysCysIleCysTyrrPheProCys 80

RESULT 5

US-09-829-381D-20

Sequence 20, Application US/09829381D

Patent No. 6653280

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yennie S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Con

TROLLING PLANT PATHOGENIC FUNGI

FILE REFERENCE: 38-21 (10700) C

CURRENT APPLICATION NUMBER: US/09/829,381D

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 09/103,489

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGTH: 80

TYPE: PRT

ORGANISM: Raphanus sativus

US-09-829-381D-20

Alignment Scores:

Pred. No.: 4,74e-44 Length: 80
Score: 434.00 Matches: 79
Percent Similarity: 98.75% Conservative: 0
Best Local Similarity: 98.75% Mismatches: 1
Query Match: 57.71% Indels: 0
DB: 4 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-829-381D-20 (1-80)

QY 16 ATGGCTAAGTTGGCTCCATCATCGCACTCTTTTGTCTCTCTTTTGTCTCTCTTTTGTCTCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaValLeuPheAlaAla 20

76	TTCTGAGCACCACCAATGCTGGAGACACAGAGTCTTGGAAAGCCCACTGGGACATG	135
Qy		
21	PheGluLaGluThrMetValGluAlaGlnLysLeuCySgluArgpTserGlyThrTrp	40
Db		
136	TCAGGAGTCTGTGGAAACAATAACGGCATCAAGAANTCAGTCATTAACTTGGAAAGCA	195
Qy		
41	SerGIyValCyGlnAsnAsnAlaCyLysAsnGlnCySileAsnLeuGluLysAla	60
Db		
196	CGACATGGATCTTGCAACTATGTCTCCCACTCACAAAGTATCTGCTACTTCTCTTGT	255
Qy		
61	ArgHisGlySerCysAsnTrpValPheProAlaHisLysCysIleCysTrpPheProCys	80
Db		

RESIST. T. 6

```

US-08-377-687-59
: Sequence 59, Application US/08377687
: Patent No. 5538525
: GENERAL INFORMATION:
: APPLICANT: BROEKAERT, WILLEM F.
: APPLICANT: CAMMUE, BRUNO P.A.
: APPLICANT: OSBORN, RUPERT W.
: APPLICANT: REES, SARAH B.
: APPLICANT: TERRAS, FRANKY R.G.
: APPLICANT: VANDERLEYDEN, JOZEFF
: TITLE OF INVENTION: BIOCIDAL PROTEINS
: NUMBER OF SEQUENCES: 59
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CUSHMAN DARBY & CUSHMAN
: STREET: 1100 NEW YORK AVENUE, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/377,687
: FILING DATE:
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/002,480
: FILING DATE: 04-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: KOKULIS, PAUL N.
: REGISTRATION NUMBER: 16,773
: REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-861-3000
: TELEFAX: 202-822-0944
: INFORMATION FOR SEQ ID NO: 59:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 80 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-377-687-59

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QY 76 TTCGAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCGCATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGATCTTGCACACTATGTCTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 8

US-08-971-982-59

; Sequence 59, Application US/08971982

; Patent No. 6187904

; GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.

; CAMMUE, BRUNO P. A.

; OSBORN, RUPERT W.

; REES, SARAH B.

; TERRAS, FRANKY R. G.

; VANDERLEIDEN, JOZEF

; TITLE OF INVENTION: BIOCIDAL PROTEINS

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARB & CUSHMAN

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/971,982

; FILING DATE: 17-No. 6187904-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/002,480

; FILING DATE: 04-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: KOKULIS, PAUL N.

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-08-971-982-59

Alignment Scores:

Pred. No.: 6,25e-44 Length: 80

Score: 433.00 Matches: 78

Percent Similarity: 98.75% Conservative: 1

Best Local Similarity: 97.50% Mismatches: 1

Query Match: 57.58% Indels: 0

DB: 3 Gaps: 0

US-10-006-252A-19 (1-414) x US-08-971-982-59 (1-80)

QY 16 ATGGCTAAGTTGCGTCCATCATCGCACTTCTTTTGTGCTTCTTTTGTGCTTCTTTTGTGCT 75

Db 1 MetAlaLysPheAlaSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20

QY 76 TTCGAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCGCATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGATCTTGCACACTATGTCTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 9

US-09-589-733C-21

; Sequence 21, Application US/09589733C

; Patent No. 6677503

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis L.

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duwick, Jon

; APPLICANT: Hu, Xu

; APPLICANT: Lu, Guihua

; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and

; FILE OF INVENTION: Genes and their Uses

; FILE REFERENCE: 5718-90

; CURRENT APPLICATION NUMBER: US/09/589,733C

; PRIOR APPLICATION NUMBER: 60/140,646

; PRIOR FILING DATE: 2000-06-08

; PRIOR FILING DATE: 1999-06-23

; PRIOR FILING DATE: 60/162,904

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: Fast-Seq for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Raphanus sativus

US-09-589-733C-21

Alignment Scores:

Pred. No.: 5,32e-42 Length: 80

Score: 417.00 Matches: 74

Percent Similarity: 95.00% Conservative: 2

Best Local Similarity: 92.50% Mismatches: 4

Query Match: 55.45% Indels: 0

DB: 4 Gaps: 0

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QY 76 TTCGAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135

Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATAAGCGCATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195

Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60

QY 196 CGACATGATCTTGCACACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255

Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 10

US-09-589-733C-23

; Sequence 23, Application US/09589733C

; Patent No. 6677503

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis L.

; APPLICANT: Crasta, Oswald R.

```
; APPLICANT: Davick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; FILE REFERENCE: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-589-733C-23

Alignment Scores:
Pred. No.: 1,38e-39      Length: 80
Score: 397.00           Matches: 70
Percent Similarity: 92.50%      Conservative: 4
Best Local Similarity: 87.50%    Mismatches: 6
Query Match: 52.79%            Indels: 0
DB: 4                      Gaps: 0

US-10-006-252A-19 (1-414) x US-09-589-733C-23 (1-80)
QY 16 ATGGCTAAAGTTTGGCTCCATCATGCACTTCTTTTCTGCTGCTGCTTTTCTGCTGCT 75
Db 1 MetAlaLysSerAlaThrIleValThrLeuPheAlaAlaLeuValPheAlaAla 20
QY 76 TTCGAAGCACCAACAAATGGTGGAGGACAGACAGAGTGTGGCAAGGCGCAAGTGGGACATGG 135
Db 21 LeuGluaLapMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGCTGTGGAAACAATAACGATGCAAGATCAGTGCATTACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysLeuAsnLeuGluLysAla 60
QY 196 CGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTGTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 11
US-08-627-706-15
; Sequence 15, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/627,706
; FILING DATE:

; APPLICANT: Davick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; FILE REFERENCE: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-589-733C-23

Alignment Scores:
Pred. No.: 1,38e-39      Length: 80
Score: 397.00           Matches: 70
Percent Similarity: 92.50%      Conservative: 4
Best Local Similarity: 87.50%    Mismatches: 6
Query Match: 52.79%            Indels: 0
DB: 4                      Gaps: 0

US-10-006-252A-19 (1-414) x US-08-627-706-15 (1-79)
QY 16 ATGGCTAAAGTTTGGCTCCATCATGCACTTCTTTTCTGCTGCTGCTTTTCTGCTGCT 75
Db 1 MetAlaLysPheAlaThrIleSerLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAAATGGTGGAGGACAGACAACTGTGCGAAGGCGCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValAspAlaA---ArgLeuCysGluArgProSerGlyThrTrp 39
QY 136 TCAGGAGCTGTGGAAACAATAACGATGCAAGATCAGTGCATTACCTTGAGAAAGCA 195
Db 40 SerGlyValCysGlyAsnSerAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTGTGT 255
Db 60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79

RESULT 12
US-09-103-489-15
; Sequence 15, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
```

REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-103-489-15

Alignment Scores:
Pred. No.: 1,58e-39
Score: 396.50
Percent Similarity: 96.25%
Best Local Similarity: 88.75%
Query Match: 52.73%
DB: 3
Gaps: 1

US-10-006-252A-19 (1-414) x US-09-103-489-15 (1-79)

QY 16 ATGGCTAAGTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaThrIleSerLeuLeuPheAlaValLeuPheAlaAa 20
QY 76 TTCGAAGCACCACAAATGGTGAAGCAGACAGAGTTGTGCGAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValaspAa--ArgLeuCysGluArgProSerGlyThrTrp 39
QY 136 TCAGAGTCTGTGGAACATACGATGCAAGATCAGTGCATTAACTTGAAGAAAGCA 195
Db 40 SerGlyValCysGlyAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 60 GluHisGlySerCysAsnTyrrValPheProAlaHisCysCysileCysTyrPheProCys 79

RESULT 13
US-09-829-381D-15
Sequence 15, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFF from Alyssum and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent in version 3.1
SEQ ID NO 15
LENGTH: 79
TYPE: PRT
ORGANISM: Alyssum Sp.
US-09-829-381D-15

Alignment Scores:
Pred. No.: 1,58e-39
Score: 396.50
Percent Similarity: 96.25%
Best Local Similarity: 88.75%
Query Match: 52.73%
DB: 4
Gaps: 1

US-10-006-252A-19 (1-414) x US-09-829-381D-15 (1-79)

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Db 1 MetAlaLysPheAlaThrIleSerLeuLeuPheAlaValLeuPheAlaAa 20
QY 76 TTCGAAGCACCACAAATGGTGAAGCAGACAGAGTTGTGCGAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValaspAa--ArgLeuCysGluArgProSerGlyThrTrp 39
QY 136 TCAGAGTCTGTGGAACATACGATGCAAGATCAGTGCATTAACTTGAAGAAAGCA 195
Db 40 SerGlyValCysGlyAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 60 GluHisGlySerCysAsnTyrrValPheProAlaHisCysCysileCysTyrPheProCys 79

RESULT 14
US-08-377-687-19
Sequence 19, Application US/08377687
Patent No. 5538525
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-377-687-19

Alignment Scores:
Pred. No.: 4,96e-29
Score: 309.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 41.09%
DB: 1
Gaps: 0

US-10-006-252A-19 (1-414) x US-08-377-687-19 (1-51)

QY 103 CAGAAGTTGTCGAAAGCCCAAGTGGACATGTCAGAGTCTGTGGAACATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGAATCAGTCAGTAACTTTCAGAAAGCAGACATGGATCTTGCAACTATGTCCTTC 222
 Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
 QY 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
 Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 15

US-08-627-706-18
 : Sequence 1B, Application US/08627706
 : Patent No. 5773696
 : GENERAL INFORMATION:
 : APPLICANT: Liang, Jihong
 : APPLICANT: Shah, Dilip M.
 : APPLICANT: Wu, Yennie S.
 : APPLICANT: Rosenberger, Cindy A.
 : TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 : TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
 : NUMBER OF SEQUENCES: 19
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 : STREET: 700 Chesterfield Village Parkway No. 5773696th
 : CITY: St. Louis
 : STATE: Missouri
 : COUNTRY: USA
 : ZIP: 63198
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/627,706
 : FILING DATE:
 : CLASSIFICATION: 436
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Cohen, Charles E.
 : REGISTRATION NUMBER: 34,565
 : REFERENCE/DOCKET NUMBER: 38-21(10700)A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (314)537-6224
 : TELEFAX: (314)537-6047
 : INFORMATION FOR SEQ ID NO: 18:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 51 amino acids
 : TYPE: amino acid
 : STRANDEDNESS:
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-627-706-18

Alignment Scores:
 Pred. No.: 4,96e-29 Length: 51
 Score: 309.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 41.09% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x US-08-627-706-18 (1-51)

QY 103 CAGAAGTTGTCGAAAGCCCAAGTGGACATGTCAGAGTCTGTGGAACATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGAATCAGTCAGTAACTTTCAGAAAGCAGACATGGATCTTGCAACTATGTCCTTC 222

Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
 QY 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
 Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

Search completed: May 11, 2004, 17:06:19
 Job time : 27 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 17:02:19 ; Search time 41.5 Seconds
(without alignments)
5537.958 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description

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3	434	57.7	80	12	US-10-681-972-20	Sequence 20, Appl
4	433	57.6	80	9	US-09-759-584-59	Sequence 59, Appl
5	417	55.5	80	12	US-10-636-396-21	Sequence 21, Appl
6	403	53.6	80	9	US-09-732-561-16	Sequence 16, Appl
7	403	53.6	80	9	US-09-732-561-22	Sequence 22, Appl
8	397	52.8	80	9	US-09-732-561-14	Sequence 14, Appl
9	397	52.8	80	12	US-10-636-396-23	Sequence 23, Appl
10	396.5	52.7	79	9	US-09-829-381A-15	Sequence 15, Appl
11	396.5	52.7	79	12	US-10-681-972-15	Sequence 15, Appl
12	309	41.1	51	9	US-09-759-584-19	Sequence 19, Appl
13	309	41.1	51	9	US-09-732-561-19	Sequence 19, Appl
14	309	41.1	51	9	US-09-829-381A-18	Sequence 18, Appl
15	309	41.1	51	12	US-10-681-972-18	Sequence 18, Appl
16	309	41.1	51	12	US-10-388-361A-34	Sequence 34, Appl
17	309	41.1	51	12	US-10-636-396-22	Sequence 22, Appl
18	309	41.1	51	13	US-10-006-252A-8	Sequence 8, Appl
19	309	41.1	51	15	US-10-072-809A-33	Sequence 33, Appl
20	309	41.1	51	15	US-10-072-809A-35	Sequence 35, Appl
21	304	40.4	51	9	US-09-732-561-17	Sequence 17, Appl
22	303	40.3	51	15	US-10-072-809A-31	Sequence 31, Appl
23	302	40.2	51	13	US-10-006-252A-58	Sequence 58, Appl
24	302	40.2	51	13	US-10-006-252A-60	Sequence 60, Appl
25	301	40.0	51	13	US-10-006-252A-57	Sequence 57, Appl
26	300	39.9	51	9	US-09-829-381A-19	Sequence 19, Appl
27	300	39.9	51	12	US-10-681-972-19	Sequence 19, Appl
28	300	39.9	51	12	US-10-388-361A-35	Sequence 35, Appl
29	300	39.9	51	13	US-10-006-252A-9	Sequence 9, Appl
30	300	39.9	51	13	US-10-006-252A-20	Sequence 20, Appl
31	300	39.9	51	13	US-10-006-252A-61	Sequence 61, Appl
32	300	39.9	51	15	US-10-072-809A-34	Sequence 34, Appl
33	296	39.4	51	13	US-10-006-252A-22	Sequence 22, Appl
34	296	39.4	51	13	US-10-006-252A-29	Sequence 29, Appl
35	295	39.2	51	13	US-10-006-252A-65	Sequence 65, Appl
36	295	39.2	51	13	US-10-006-252A-39	Sequence 39, Appl
37	295	39.2	51	13	US-10-006-252A-31	Sequence 31, Appl
38	295	39.2	51	13	US-10-006-252A-44	Sequence 44, Appl
39	295	39.2	51	13	US-10-006-252A-77	Sequence 77, Appl
40	294	39.1	51	13	US-10-006-252A-28	Sequence 28, Appl
41	294	39.1	51	13	US-10-006-252A-41	Sequence 41, Appl
42	294	39.1	51	13	US-10-006-252A-42	Sequence 42, Appl
43	294	39.1	51	13	US-10-006-252A-59	Sequence 59, Appl
44	293	39.0	51	13	US-10-006-252A-23	Sequence 23, Appl
45	293	39.0	51	13	US-10-006-252A-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-759-584-49
; Sequence 49, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMUE, BRUNO P.A.
; APPLICANT: OSBORN, ROBERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-759-584-49

Alignment Scores:
Pred. No.: 7,57e-42 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.78% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-759-584-49 (1-80)

QY 16 ATGGCTAAGTTGGCTGCATCATCGCACTTCTTTTGGCTGCTGCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGTGGGAAGCACAGAGTTGTGGGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCATGCAAGATCAGTCAATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGATCTTCAACTATGCTTCCAGCTCACAAGTATGCTACTTTCCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 2

US-09-829-381A-20
Sequence 20, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal polypeptide and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-829-381A-20

Alignment Scores:
Pred. No.: 6,28e-41 Length: 80
Score: 434.00 Matches: 79
Percent Similarity: 98.75% Conservative: 0
Best Local Similarity: 98.75% Mismatches: 1
Query Match: 57.71% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-829-381A-20 (1-80)

QY 16 ATGGCTAAGTTGGCTGCATCATCGCACTTCTTTTGGCTGCTGCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGTGGGAAGCACAGAGTTGTGGGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCATGCAAGATCAGTCAATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGATCTTCAACTATGCTTCCAGCTCACAAGTATGCTACTTTCCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3

US-10-681-972-20
Sequence 20, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal polypeptide ALYAP from Alyssum and Methods for Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

ORGANISM: Raphanus sativus
US-10-681-972-20

Alignment Scores:
Pred. No.: 6,28e-41 Length: 80
Score: 434.00 Matches: 79
Percent Similarity: 98.75% Conservative: 0
Best Local Similarity: 98.75% Mismatches: 1
Query Match: 57.71% Indels: 0
DB: 12 Gaps: 0

US-10-006-252A-19 (1-414) x US-10-681-972-20 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGGTGGAGACACAGATTGTGGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGAGTCTGTGGAACAATAAAGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLysLeuGluLysAla 60
QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTGATCTGCTACTTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 4

US-09-759-584-59
Sequence 59, Application US/09759584
Patent No. US20010014732A1

GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-759-584-59

Alignment Scores:
Pred. No.: 8,18e-41 Length: 80
Score: 433.00 Matches: 78
Percent Similarity: 98.75% Conservative: 1
Best Local Similarity: 97.50% Mismatches: 1
Query Match: 57.58% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-759-584-59 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGGTGGAGACACAGATTGTGGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGAGTCTGTGGAACAATAAAGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLysLeuGluLysAla 60
QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTGATCTGCTACTTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 5

US-10-636-396-21
Sequence 21, Application US/10636396
Publication No. US20040073971A1

GENERAL INFORMATION:
APPLICANT: BIDNEY, DENNIS L.
APPLICANT: CRASTA, OSWALD R.
APPLICANT: DUVICK, JON
APPLICANT: HU, XU
APPLICANT: LU, GUIHUA
TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and Genes and their Uses
FILE REFERENCE: 5718-90
CURRENT APPLICATION NUMBER: US/10/636,396
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: US/09/589,733C
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/162,904
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 80
TYPE: PRT
ORGANISM: Raphanus sativus

US-10-636-396-21

Alignment Scores:
Pred. No.: 5,62e-39 Length: 80
Score: 417.00 Matches: 74
Percent Similarity: 95.00% Conservative: 2
Best Local Similarity: 92.50% Mismatches: 4
Query Match: 55.45% Indels: 0
DB: 12 Gaps: 0

US-10-006-252A-19 (1-414) x US-10-636-396-21 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGGTGGAGACACAGATTGTGGAAAGGCCAAGTGGACATGG 135

Db 21 PheGluGluProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 Qy 136 TCAGGAGTCTGGGAACAATAACCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 60
 Qy 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAAGTGATCTGCTACTTTCCTTCT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 6

US-09-732-561-16
 ; Sequence 16, Application US/09732561
 ; Patent No. US20020035738A1

GENERAL INFORMATION:

APPLICANT: Thoma, Bart
 APPLICANT: Terras, Franky
 APPLICANT: Penninckx, Iris
 APPLICANT: Manners, John
 APPLICANT: Kazan, Kemal
 APPLICANT: Broekaert, Willem
 TITLE OF INVENTION: Plant Protection Method
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA AG Products
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/732,561
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/202,638
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB97/01672
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 REFERENCE/DOCKET NUMBER: PPD 50165/UST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-1699
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 STRAIN: PDF 1.2

US-09-732-561-16

Alignment Scores:
 Pred. No.: 2,28e-37 Length: 80
 Score: 403.00 Matches: 71
 Percent Similarity: 95.00% Conservative: 5
 Best Local Similarity: 88.75% Mismatches: 4
 Query Match: 53.59% Indels: 0
 DB: 9 Gaps: 0

US-10-006-252a-19 (1-414) x US-09-732-561-16 (1-80)

Qy 16 ATGGCTAGTTCGTCACATCGCAGCTCTTTTTCCTGCTCTCTTTTTCCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleIleThrLeuIlePheAlaLeuValLeuPheAlaAla 20
 Qy 76 TTCGAGGACCAACCAATAGTGGAAAGCACAGAAGTTGTGCGAAAGCCAAAGTGGACATGG 135
 Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGlnLysProSerGlyThrTrp 40
 Qy 136 TCAGGAGTCTGGGAACAATAACCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 60
 Qy 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAAGTGATCTGCTACTTTCCTTCT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 7

US-09-732-561-22
 ; Sequence 22, Application US/09732561
 ; Patent No. US20020035738A1

GENERAL INFORMATION:

APPLICANT: Thoma, Bart
 APPLICANT: Terras, Franky
 APPLICANT: Penninckx, Iris
 APPLICANT: Manners, John
 APPLICANT: Kazan, Kemal
 APPLICANT: Broekaert, Willem
 TITLE OF INVENTION: Plant Protection Method
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA AG Products
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/732,561
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/202,638
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB97/01672
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 REFERENCE/DOCKET NUMBER: PPD 50165/UST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-1699
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 STRAIN: Arabidopsis PDF1.2 amino acid sequence

US-09-732-561-22

Alignment Scores:
 Pred. No.: 2,28e-37 Length: 80
 Score: 403.00 Matches: 71
 Percent Similarity: 95.00% Conservative: 5
 Best Local Similarity: 88.75% Mismatches: 4

Query Match: 53.59% Indels: 0
 DB: 9 Gaps: 0
 US-10-006-252A-19 (1-414) x US-09-732-561-22 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTCTGCTCTTTTGGCTGT 75
 Db 1 MetAlaLysPheAlaSerIleThrLeuPheAlaAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCAACAATGGTGGAAAGCAGAGTGTGCGAAAGGCCAAGTGGGACATG 135
 Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGAGTCTGTGGAACAATACGCATGCAAGATCAGTGCATTAACTTGGAGAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
 RESULT 8
 US-09-732-561-14
 ; Sequence 14, Application US/09732561
 ; Patent No. US20020035738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thoma, Bart
 ; APPLICANT: Terras, Franky
 ; APPLICANT: Penninckx, Iris
 ; APPLICANT: Manners, John
 ; APPLICANT: Kazan, Kemal
 ; APPLICANT: Broekaert, Willem
 ; TITLE OF INVENTION: Plant Protection Method
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZENECA Ag Products
 ; STREET: 1800 Concord Pike
 ; CITY: Wilmington
 ; STATE: DE
 ; COUNTRY: USA
 ; ZIP: 19850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/732,561
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/202,638
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GE97/01672
 ; FILING DATE: 20-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hohenschutz, Liza D.
 ; REGISTRATION NUMBER: 33,712
 ; REFERENCE/DOCKET NUMBER: PPD 50165/UST
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 886-1699
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 80 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; STRAIN: PDF1.1
 US-09-732-561-14

Alignment Scores:
 Pred. No.: 1,11e-36 Length: 80
 Score: 397.00 Matches: 70
 Percent Similarity: 92.50% Conservative: 4
 Best Local Similarity: 87.50% Mismatches: 6
 Query Match: 52.79% Indels: 0
 DB: 9 Gaps: 0
 US-10-006-252A-19 (1-414) x US-09-732-561-14 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTCTGCTCTTTTGGCTGT 75
 Db 1 MetAlaLysSerAlaThrIleValThrLeuPheAlaAlaLeuValPheAlaAla 20
 QY 76 TTCGAAGCACCAACAATGGTGGAAAGCAGAGTGTGCGAAAGGCCAAGTGGGACATG 135
 Db 21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGAGTCTGTGGAACAATACGCATGCAAGATCAGTGCATTAACTTGGAGAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
 RESULT 9
 US-10-636-396-23
 ; Sequence 23, Application US/10636396
 ; Publication No. US20040073971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bidney, Dennis L.
 ; APPLICANT: Crasta, Oswald R.
 ; APPLICANT: Duvick, Jon
 ; APPLICANT: Hu, Xu
 ; APPLICANT: Lu, Guihua
 ; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
 ; TITLE OF INVENTION: Genes and their Uses
 ; FILE REFERENCE: 5718-90
 ; CURRENT APPLICATION NUMBER: US/10/636,396
 ; CURRENT FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: US/09/589,733C
 ; PRIOR FILING DATE: 2000-06-08
 ; PRIOR APPLICATION NUMBER: 60/140,646
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/162,904
 ; PRIOR FILING DATE: 1999-11-01
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 80
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-636-396-23
 Alignment Scores:
 Pred. No.: 1,11e-36 Length: 80
 Score: 397.00 Matches: 70
 Percent Similarity: 92.50% Conservative: 4
 Best Local Similarity: 87.50% Mismatches: 6
 Query Match: 52.79% Indels: 0
 DB: 12 Gaps: 0
 US-10-006-252A-19 (1-414) x US-10-636-396-23 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTCTGCTCTTTTGGCTGT 75
 Db 1 MetAlaLysSerAlaThrIleValThrLeuPheAlaAlaLeuValPheAlaAla 20
 QY 76 TTCGAAGCACCAACAATGGTGGAAAGCAGAGTGTGCGAAAGGCCAAGTGGGACATG 135
 Db 21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATACCATGCAAGATCAGTGCATTAACCTTGGAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysLeuAsnLeuGluLysAla 60
 QY 196 CGACATGATCTTGCACAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTCTCTGT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysileCysTyrPheProCys 80

RESULT 10

US-09-829-381A-15
 ; Sequence 15, Application US/09829381A
 ; Patent No. US20020144306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yennie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 ; Controlling Plant Pathogenic Fungi
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 ; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: US/09/829,381A
 ; APPLICATION NUMBER: US/09/829,381A
 ; FILING DATE: 09-Apr-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/103,489
 ; FILING DATE: 1998-06-24
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cohen, Charles E.
 ; REGISTRATION NUMBER: 34,565
 ; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 537-6224
 ; TELEFAX: (314) 537-6047
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 79 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-829-381A-15
 Alignment Scores:
 Pred. No.: 1,27e-36 Length: 79
 Score: 396.50 Matches: 71
 Percent Similarity: 96.25% Conservative: 6
 Best Local Similarity: 88.75% Mismatches: 2
 Query Match: 52.73% Indels: 1
 DB: 9 Gaps: 1

US-10-006-252A-19 (1-414) x US-09-829-381A-15 (1-79)

QY 16 ATGGTAAGTTGGTGCATCATCGCACTTCTTTTGTGCTCTGTTCTTTTCTGCT 75
 Db 1 MetAlaLysPheAlaThrIleSerLeuPheAlaAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCAACAATGCTGGAAGCACAGAGTTGCGAAGCCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProThrMetValAspAla--ArgLeuCysGluArgProSerGlyThrTrp 39

QY 136 TCAGGAGTCTGTGGAACAATACCATGCAAGATCAGTGCATTAACCTTGGAAGCA 195
 Db 40 SerGlyValCysGlyAsnSerAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
 QY 196 CGACATGATCTTGCACAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTCTGT 255
 Db 60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysileCysTyrPheProCys 79

RESULT 11

US-10-681-972-15
 ; Sequence 15, Application US/10681972
 ; Publication No. US20040064850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yennie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
 ; TITLE OF INVENTION: Plant Pathogenic Fungi
 ; FILE REFERENCE: 38-21 (10700) C
 ; CURRENT APPLICATION NUMBER: US/10/681,972
 ; PRIOR FILING DATE: 2003-10-09
 ; PRIOR APPLICATION NUMBER: US/09/829,381D
 ; PRIOR FILING DATE: 2001-04-09
 ; PRIOR APPLICATION NUMBER: 09/103,489
 ; PRIOR FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15
 ; LENGTH: 79
 ; TYPE: PPT
 ; ORGANISM: Alyssum Sp.
 ; US-10-681-972-15

Alignment Scores:
 Pred. No.: 1,27e-36 Length: 79
 Score: 396.50 Matches: 71
 Percent Similarity: 96.25% Conservative: 6
 Best Local Similarity: 88.75% Mismatches: 2
 Query Match: 52.73% Indels: 1
 DB: 12 Gaps: 1

US-10-006-252A-19 (1-414) x US-10-681-972-15 (1-79)

QY 16 ATGGTAAGTTGGTGCATCATCGCACTTCTTTTGTGCTCTGTTCTTTTCTGCT 75
 Db 1 MetAlaLysPheAlaThrIleSerLeuPheAlaAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCAACAATGCTGGAAGCACAGAGTTGCGAAGCCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProThrMetValAspAla--ArgLeuCysGluArgProSerGlyThrTrp 39
 QY 136 TCAGGAGTCTGTGGAACAATACCATGCAAGATCAGTGCATTAACCTTGGAAGCA 195
 Db 40 SerGlyValCysGlyAsnSerAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
 QY 196 CGACATGATCTTGCACAACTATGCTTCCAGCTCACAAAGTGTATCTGCTACTTCTGT 255
 Db 60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysileCysTyrPheProCys 79

RESULT 12

US-09-759-584-19
 ; Sequence 19, Application US/09759584
 ; Patent No. US20010014732A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKAERT, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERZAS, FRANKY R.G.
 ; APPLICANT: VANDERLEYDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-759-584-19

Alignment Scores:
Pred. No.: 1.28e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) X US-09-759-584-19 (1-51)

QY 103 CAGAGTTGTGCGAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAla 20
QY 163 TCGAAGATCAGTGCATTACCTTGAGAAAGCACACATGGATCTTGCACATATCTCTTC 222
Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTrpValPhe 40
QY 223 CCAGCTCACAGTGTATCTGCTACTTCTCTTGT 255
Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 13

US-09-732-561-19
Sequence 19, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Thoma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Ag Products

STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: Rs-AFP1
US-09-732-561-19

Alignment Scores:
Pred. No.: 1.28e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) X US-09-732-561-19 (1-51)
QY 103 CAGAGTTGTGCGAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
QY 163 TCGAAGATCAGTGCATTACCTTGAGAAAGCACACATGGATCTTGCACATATCTCTTC 222
Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTrpValPhe 40
QY 223 CCAGCTCACAGTGTATCTGCTACTTCTCTTGT 255
Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 14

US-09-829-381A-18
Sequence 18, Application US/09829381A
Patent No. US2002014306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-829-381A-18

Alignment Scores:
Pred. No.: 1.28e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-829-381A-18 (1-51)

Qy	103	CAGAAGTTGTGCGAAGCCGAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCA	162
Db	1	GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla	20
Qy	163	TGCAGAAATCACTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTC	222
Db	21	CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe	40
Qy	223	CCAGCTCACAGTGTATCTGCTACTTTCCTTGT	255
Db	41	ProAlaHisLysCysIleCysTy-PheProCys	51

RESULT 15

US-10-681-972-18
Sequence 18, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide AlyAPP from Alyseum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489

PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 51
TYPE: PRT
ORGANISM: Raphanus sativus
US-10-681-972-18
Alignment Scores:
Pred. No.: 1.28e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 12 Gaps: 0
US-10-006-252A-19 (1-414) x US-10-681-972-18 (1-51)
Qy 103 CAGAAGTTGTGCGAAGCCGAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
Qy 163 TGCAGAAATCACTGCAATTAACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTC 222
Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
Qy 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db 41 ProAlaHisLysCysIleCysTy-PheProCys 51
Search completed: May 11, 2004, 17:07:51
Job time : 42.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:59:19 ; Search time 18.5 Seconds
(without alignments)
4305.221 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 752
Sequence: 1 gttttattagtcattggc.....caaaaaaaaaaaaaaaaaa 414

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool_p/US10006252/runat_11052004_141658_22811/app_query.fasta_1.583
-DB=PIR_78 -QMT-fastan -SUFIX=PIR -MINMATCH=0.1 -LOPCU=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006252@cgn 1.1.38 @runat_11052004_141658_22811 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	442	58.8	80	T10176	antifungal protein
2	417	55.5	80	T10823	antifungal protein
3	405	53.9	80	T10183	antifungal protein
4	400	53.2	80	T02621	probable antifunga
5	399	53.1	80	T02622	antifungal protein
6	397	52.8	80	T02622	antifungal protein
7	394.5	52.5	79	T07917	protein T4O12.7 [i
8	393.5	52.3	79	T10243	antifungal protein
9	207	27.5	80	T02621	probable antifunga
10	175	23.3	30	T28991	antifungal protein
11	164	21.8	56	G83328	hypothetical prote
12	161	21.4	27	S28989	antifungal protein
13	156	20.7	27	S28995	antifungal protein
14	154	20.5	50	S66221	defensin AMP1 - Da

15	151	20.1	25	2	S28993	antifungal protein
16	149	19.8	26	2	S28994	antifungal protein
17	149	19.8	161	2	S12246	anther-specific pr
18	146.5	19.5	50	2	S66218	defensin AMP1 - Ae
19	145.5	19.3	49	2	S66219	defensin AMP1 - Cl
20	145.5	19.3	54	2	S66220	defensin AMP1 - He
21	142	18.9	27	2	S28990	antifungal protein
22	141.5	18.8	105	2	S57809	gamma-thionin-like
23	115	15.3	83	2	T14866	probable gamma-thi
24	114	15.2	105	2	S23574	thionin precursor,
25	113	15.0	152	2	S46272	anther-specific pr
26	110.5	14.7	83	2	T03673	pit1 protein (clon
27	99	13.2	73	2	D84433	proteinase inhibit
28	95	12.6	75	2	S11156	PSA10 protein - c
29	93.5	12.4	74	2	T02667	disease resistance
30	91.5	12.2	81	2	T02667	proteinase inhibit
31	90.5	12.1	380	2	T04508	hypothetical prote
32	87.5	11.6	72	2	T06599	disease resistance
33	83	11.0	77	2	C84433	proteinase inhibit
34	82.5	11.1	221	2	T22771	hypothetical prote
35	82	10.9	77	2	S30578	protease inhibitor
36	81.5	10.8	79	2	T06381	proteinase inhibit
37	81	10.8	82	2	JC7897	defensin 1 precurs
38	80	10.6	77	2	B84433	proteinase inhibit
39	80	10.6	833	2	S19087	gene Delta protein
40	79	10.5	77	2	T14395	proteinase inhibit
41	79	10.5	768	2	I53821	P-selectin - rat
42	79	10.5	832	2	A31246	neurogenic protein
43	79	10.5	880	2	S00670	neurogenic repetit
44	77.5	10.3	467	2	S30839	UTR2 protein - yea
45	77	10.2	121	2	S17718	anther-specific pr

ALIGNMENTS

RESULT 1

T10176

antifungal protein 1 precursor - radish

C/Species: Raphanus sativus (radish)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000

C/Accession: T10176; A42842

R/Terras, P.R.; Eggermont, K.; Kovaleva, V.; Raikhel, N.V.; Osborn, R.W.; Kester, A.

Plant Cell 7, 568-573, 1995

A/Title: Small cysteine-rich antifungal proteins from radish: their role in host def.

A/Reference number: Z16976

A/Accession: T10176

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-80 <TER>

A/Cross-references: EMBL:U18557; NID:G644773; PID:G609322

A/Experimental source: strain ronde rode kline witpunt; tissue type seed

R/Terras, P.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderley;

J. Biol. Chem. 267, 15301-15309, 1992

A/Title: Analysis of two novel classes of plant antifungal proteins from radish (Rapi

A/Reference number: A42842; MUID:92348373; PMID:1639777

A/Accession: A42842

A/Status: preliminary

A/Molecule type: protein

A/Residues: 30-73 <TE2>

A/Experimental source: seed

A/Note: sequence extracted from NCBI backbone (NCBI:109570)

C/Genetics:

A/Gene: APPI

C/Function:

A/Description: involved in creation of a microenvironment around the seed in which fi

A/Note: preferentially released during seed germination

C/Superfamily: gamma-thionin

C/Keywords: antifungal

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-80/Product: antifungal protein 1 #status predicted <MAT>

Alignment Scores:

Pred. No.: 1.8e-39 Length: 80

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Db      21 PheGluGluProThrMetValGluAlaGlnLeuCySglnArgProSerGlyThrTrp 40
QY     136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAANTCACTGCAATTAACCTTGAAGAAGCA 195
Db      41 SerGlyValCySgLYAsnAsnAlaCySlyAsnGlnCysIleAArgLeuGluLYeAla 60
QY     196 CGACATGATCTTGCAACTATGTCTTCCCAAGCTCACAAGTGTATCTGCTACTCTTCCCTTGT 255
Db      61 ArgHisGlySerCyAsnTyrrValPheProAlaHisLYeCySilleCySlyrPheProCys 80

RESULT 3
Tt0183
antifungal protein 4 precursor - radish
C.Species: Raphanus sativus (radish)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C.Accession: Tt0183
R.Terras, F.R.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z16981
A:Accession: Tt0183
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-80 <TER>
A:Cross-references: EMBL:X97318
A:Experimental source: cultivar Ronde Rode Kleine Witput
C:Genetics:
C:Gene: AP4
C:Superfamily: gamma-thionin
C.Keywords: antifungal
F.1-29/Domain: signal sequence #status predicted <SIG>
F.30-80/Product: antifungal protein 4 #status predicted <MAT>

Alignment Scores:
Pred. No.: 1,82e-35 Length: 80
Score: 405.00 Matches: 72
Percent Similarity: 92.50% Conservative: 2
Best Local Similarity: 90.00% Mismatches: 6
Query Match: 53.86% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x Tt0183 (1-80)

QY     16 ATGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTGCTTGTCTTTTGTGCTGT 195
Db      1 MetAlaLYePheValSerIleIleThrLeuLeuPheValAlaLeuValLeuPheAlaAla 20
QY     76 TTCGAAGCACCAACAAATGGTGGAGCACAGAAGTTGTGCGAAGGCCCAAGTGGGCATGG 135
Db      21 PheGluAlaProThrMetValGluAlaGlnLYeLeuCySGLuAGSerSerGlyThrTrp 40
QY     136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCACTGCAATTAACCTTGAAGAAGCA 195
Db      41 SerGlyValCySgLYAsnAsnAlaCySlyAsnGlnCysIleAAsnLeuGluLYeAla 60
QY     196 CGACATGATCTTGCAACTATGTCTTCCCAAGCTCACAAGTGTATCTGCTACTCTTCCCTTGT 255
Db      61 ArgHisGlySerCyAsnTyrrIlePheProTyrrHisAGCySilleCySlyrPheProCys 80

RESULT 4
Tt0621
probable antifungal protein Tt9L18.17 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C.Accession: T02621; E04655
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC Tt9L18 genomic sequence.
A:Reference number: Z14681
A:Accession: T02621
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-80 <ROU>

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A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413721
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: E84655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE002093; NID:g3413721; PIDN:AAC31244.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: Atg26020; T19L18.17
 A;Map position: 2
 A;Introns: 22/1
 C;Superfamily: gamma-thionin

Alignment Scores:
 Pred. No.: 6.32e-35 Length: 80
 Score: 400.00 Matches: 70
 Percent Similarity: 93.75% Conservative: 5
 Best Local Similarity: 87.50% Mismatches: 5
 Query Match: 53.19% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x T02621 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCGCACCTCTTTTGGCTGCTGCTTTTCTGCTGCT 75
 Db 1 MetAlalysPheAlaSerIleThrPheIleThrPheAlaLeuValLeuPheAlaA 20
 QY 76 TTCGAGCACCAACAATGGTGGAGCACAGAGTTGTGGCAAGCCAAAGTGGGACATGG 135
 Db 21 PheGluValProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGGAGTCGTGGAAACATAACGATCAGCAATCATGTCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 5

T02622
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
 C;Accession: T02622; D84655
 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, August 1998
 A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
 A;Reference number: Z14681
 A;Accession: T02622
 A;Status: translated from GB/EMBL/DBSJ
 A;Molecule type: DNA
 A;Residues: 1-80 <ROU>

A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413711
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: D84655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE002093; NID:g3413711; PIDN:AAC31234.1; GSPDB:GN00139
 C;Genetics:

A;Gene: Atg26010; T19L18.18
 A;Map position: 2
 A;Introns: 22/1
 C;Superfamily: gamma-thionin

Alignment Scores:
 Pred. No.: 8.11e-35 Length: 80
 Score: 399.00 Matches: 71
 Percent Similarity: 93.75% Conservative: 4
 Best Local Similarity: 88.75% Mismatches: 5
 Query Match: 53.06% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x T02622 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCGCACCTCTTTTGGCTGCTGCTTTTCTGCTGCT 75
 Db 1 MetAlalysSerAlaAlaIleThrPheLeuPheAlaAlaLeuValLeuPheAlaA 20
 QY 76 TTCGAGCACCAACAATGGTGGAGCACAGAGTTGTGGCAAGCCAAAGTGGGACATGG 135
 Db 21 PheGluAlaProIleMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGGAGTCGTGGAAACATAACGATCAGCAATCATGTCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 6

F96787
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C;Accession: F96787
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: F96787
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE005173; NID:g6721100; PIDN:AAF26754.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: T4012.7
 A;Map position: 1
 C;Superfamily: gamma-thionin

Alignment Scores:

Pred. No.: 1.33e-34 Length: 80
 Score: 397.00 Matches: 70
 Percent Similarity: 92.50% Conservative: 4
 Best Local Similarity: 87.50% Mismatches: 6
 Query Match: 52.79% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x F96787 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCGCACCTCTTTTGGCTGCTGCTTTTCTGCTGCT 75
 Db 1 MetAlalysSerAlaThrIleValThrPhePheAlaAlaLeuValPheAlaA 20
 QY 76 TTCGAGCACCAACAATGGTGGAGCACAGAGTTGTGGCAAGCCAAAGTGGGACATGG 135

```

Db      21  LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Qy      136  TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db      41  SerGlyValCysGlyAsnSerAsnAlaCysAsnGlnCysIleAsnLeuGluLysAla 60
Qy      196  CGACATGGATCTTGAACATATCTCTCCAGCTCACAGAGTCTATCTGCTACTTCTCTTCT 255
Db      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 7
T07917
antifungal protein - rape
C:Species: Brassica napus (rape)
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jun-2000
C:Accession: T07917
R:Schm, U.; Lee, C.M.; Lee, M.H.; Kim, J.H.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z16214
A:Accession: T07917
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-79 <SOH>
A:Cross-references: EMBL:U59459; NID:gl399229; PIDN:AB03224.1; PID:gl399230
A:Experimental source: cv. Naehan
C:Superfamily: gamma-thionin

Alignment Scores:
Pred. No.: 2,49e-34 Length: 79
Score: 394.50 Matches: 73
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 91.25% Mismatches: 4
Query Match: 52.46% Indels: 1
DB: 2 Gaps: 1

US-10-006-252A-19 (1-414) x T07917 (1-79)

Qy      16  ATGGCTAAGTTTGGCTCCATCATGCACTCTCTTTTGGCTCTCTTTTGGCTGCT 75
Db      1  MetAlaLysPheAlaSerIleLeuLeuPheAlaLeuValValPheAlaAla 20
Qy      76  TTCGAAGCACCAATCGTGGAGCGACAGAGTTGTGCGAAGCCAGTGGGACATGG 135
Db      21  PheGluAlaProThrValValGluAla---LysLeuCysGluArgSerGlyThrTrp 39
Qy      136  TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db      40  SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 59
Qy      196  CGACATGGATCTTGAACATATCTCTCCAGCTCACAGAGTCTATCTGCTACTTCTCTTGT 255
Db      60  GlnHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79

RESULT 8
T10243
antifungal protein 3 precursor - radish
C:Species: Raphanus sativus (radish)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T10243
R:Terras, F.R.G.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z16994
A:Accession: T10243
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-79 <TER>
A:Cross-references: EMBL:X97319
A:Experimental source: cultivar Ronde Rode Kleine Witpunt
C:Genetics:
A:Gene: AFP3
C:Superfamily: gamma-thionin
C:Keywords: antifungal

```

F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-79/Product: antifungal protein 3 #status predicted <MAT>

Alignment Scores:
Pred. No.: 3.2e-34 Length: 79
Score: 393.50 Matches: 72
Percent Similarity: 95.00% Conservative: 4
Best Local Similarity: 90.00% Mismatches: 3
Query Match: 52.33% Indels: 1
DB: 2 Gaps: 1

US-10-006-252A-19 (1-414) x T10243 (1-79)

```

Qy      16  ATGGCTAAGTTTGGCTCCATCATGCACTCTCTTTTGGCTCTCTTTTGGCTGCT 75
Db      1  MetAlaLysPheAlaSerIleValAlaLeuPheAlaLeuValValPheAlaAla 20
Qy      76  TTCGAAGCACCAATCGTGGAGCGACAGAGTTGTGCGAAGCCAGTGGGACATGG 135
Db      21  PheGluAlaProThrValValGluAla---LysLeuCysGluArgSerGlyThrTrp 39
Qy      136  TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db      40  SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 59
Qy      196  CGACATGGATCTTGAACATATCTCTCCAGCTCACAGAGTCTATCTGCTACTTCTTGT 255
Db      60  GlnHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79

```

RESULT 9

P96591
Probable antifungal protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: F96591

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.A.; Li, J.H.; Liu, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maizli, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96591

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-80 <STO>

A:Cross-references: GB:AE05173; NID:99857525; PIDN:AAG00880.1; GSPDB:GN00141

C:Genetics:

A:Gene: T24C10.12

A:Map position: 1

C:Superfamily: gamma-thionin

Alignment Scores:

Pred. No.: 4.93e-14 Length: 80
Score: 207.00 Matches: 40
Percent Similarity: 67.90% Conservative: 15
Best Local Similarity: 49.38% Mismatches: 24
Query Match: 27.53% Indels: 2
DB: 2 Gaps: 2

US-10-006-252A-19 (1-414) x F96591 (1-80)

```

Qy      16  ATGGCTAAGTTTGGCTCCATCATGCACTCTCTTTTGGCTCTCTTTTGGCTGCT 75
Db      1  MetAlaLysPheCysThrThrLeuLeuValAlaLeuValValPheAlaAsp 20
Qy      76  TTCGAGGCCAACCAATCGTGGAGCGACAGAGTTGTGCGAAGCCAGTGGGACATGG 135
Db      21  PheGluAlaProThrIleValLysAlaGlu---LeuCysLysArgLysSerGlyThrTrp 39

```

136	TCAGAGTCTGTGGAACACATACGCATGCAAGATCAGTGCATTAACTCTTGAGAAACCA	195
Qy		
140	SerGlyArgCysValAsnAspTyrGlnCysAgaSpHisCysIleAsnAsnAspArgGly	59
Db		
146	CGACATGGATCTTCGAACACTATGCTTCCCGAGCTCACAAAG--TGTATCTGCTACTTTCTCT	252
Qy		
150	AsnAspGlyTyrCysAlaGlyGlyTyrProTyrArgSerCyspheCyspheSer	79
Db		
253	TGT 255	
Qy		
80	Cys 80	
Db		

RESULT 10

S28991 antifungal protein 1 - rape (fragment)
C:Species: Brassica napus (rape)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C:Accession: S28991; S28992
R:Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, B.E.S. Lett. 316, 233-240, 1993
A:Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
A:Reference number: S28989; MUID:93138130; PMID:9422949
A:Accession: S28991
A:Molecule type: protein
A:Residues: 1-30 <TER>
A:Accession: S28992
A:Molecule type: protein
A:Residues: 1-23 <TE2>
C:Superfamily: gamma-thionin

Alignment Scores:	1.58e-10	Length:	30
Pred. No.:	175.00	Matches:	30
Score:	100.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	23.27%	Gaps:	0
DB:	2		

US-10-006-252A-19 (1-414) x S28991 (1-30)

QY	103	CAGAACTTTGGAAAGCCAGTCGGAGACATGTCAGGAGTCTGTGGAAACATTAACGCA	162
Db	1	GLNLSLUCYCGSLUAGrroSerGLYThrTrpSerGLYValCysGLYASNAASNAIA	20
QY	163	TGCAAGAATCAGTCGATTAACCTTGAGAAA	192
Db	21	CysLYsAsnGLNcysIleAsnLeuGLULys	30

RESULT 11
G86328
hypothetical protein Flap1.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: G86328
R:R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Huizlar, L.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luccs, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-56 <STO>
A:Cross-references: GB:AE005172; NID:G9795584; PIDN:NAF98402.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Alignment Scores:	
Pred. NO.:	2.31e-09
Score:	164.00
Matches:	56
Conservative:	7
Mismatches:	18
Indels:	0
Gaps:	0
DB:	2
Query Match:	2.81%
Best Local Similarity:	50.00%
Percent Similarity:	64.00%
Score:	164.00
Pred. NO.:	2.31e-09

US-10-006-252A-19 (1-414) x G86328 (1-56)

	QY	106	AAGTTGTGCGAAAGCCCAAGTGGACATGTGCAGGAGTCGTGGAAAACAATAACGCATGC	165
		:	: : : : : : : :	:
	Db	7	ArgIleCysGlukArgSerLysThrTrpThrGlyPheCysGlyAsnThrArgGlyCys	26
		:	: :~::~:: : : : : : : :	:
	QY	166	ARGAATCATCTGCATTAAACCTTGAAAAACGACATGGATCTTGCACATATGTCCTGCCA	225
		:	::: : : : : : : :	:
	Db	27	AspSerGlnCysLysArgTgrPluArgAlaSerHisGlyAlaCysHisAlaGlnPhePro	46
		:	: : : : : : : :	:
	QY	226	GCTCACAGTGTATCTGCTACTTTCCTTGT	255
		:	: : : : : : :	:
	Db	47	GlyPheAlaCysPheCystyrPheasnCys	56

RESULT 12

S28989
antifungal protein 1 - turnip (fragment)
C:Species: Brassica rapa (turnip)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C:Accession: S28989
R:Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.
FEBS Lett. 316, 233-240, 1993
A:Title: A new family of basic cysteine-rich plant antifungal proteins from *Brassica napus*.
A:Reference number: S28989; MUID:93138130; PMID:8423949
A:Accession: S28989
A:Molecule type: protein
A:Residues: 1-27 <TER>
C:Superfamily: gamma-thionin

Alignment Scores:	
Pred. No.:	5.24e-09
Score:	161.00
Length:	27
Matches:	27
Conservative:	0
Mismatches:	0
Best Local Similarity:	100.00%
Query Match:	21.41%
DB:	2
Gaps:	0
Indels:	0

US-10-006-252A-19 (1-414) x S28989 (1-27)

Qy	103	CACAATTCTGCGAAGCCCACTGGGACATGCTCAGGAGTCTCTGGAAACAATAACGCA	152
Db	1	GlNLYsLeuCYsGluA-gPcSerGlyThrTpSerGlyValCYsGlyAsnAsnAla	20
Qy	163	TGCAAGATCAGTCGATTAAAC	183
Db	21	CysLYsAsnGlnCysIleAsn	27

RESULT 13

S28995

antifungal protein 1 - *Arabidopsis thaliana* (fragment)

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000

C:Accession: S28995

C:Author: R.Terras, P.R.G.: Torrekens, S.; van Leeuwen, F.; Vanderleyden, J.

A:Title: A new family of basic cysteine-rich plant antifungal proteins from *Br...*

A:Reference number: S28989; MUID:33138130; PMID:8422949

A:Accession: S28995

A:Molecule type: protein

A:Residues: 1-27 <TER>

C:Superfamily: gamma-thionin

Alignment Scores:	
Pred. No.:	1.82e-08
Length:	27

Score: 156.00 Matches: 26
Percent Similarity: 100.00%
Best Local Similarity: 96.30%
Query Match: 20.74%
DB: 2

US-10-006-252A-19 (1-414) x S28993 (1-27)

Qy 103 CAGAACTTGTGCGAAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnSerAsnAla 20
Qy 163 TGCAGAAATCAGTCGATTAAAC 183
Db 21 CysLysAsnGlnCysIleAsn 27

RESULT 14

S66221
Defensin AMP1 - Dahlia merckii
N;Alternate names: seed antifungal protein
C;Species: Dahlia merckii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66221
R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven
FEBS Lett. 368, 257-262, 1995
A;Title: Isolation and characterisation of plant defensins from seeds of Asteraceae, Fab
A;Reference number: S66218; MUID:95354848; PMID:7628617
A;Molecule type: protein
A;Accession: S66221
A;Residues: 1-50 <OSB>
C;Keywords: antifungal

Alignment Scores:

Pred. No.: 2,82e-08 Length: 50
Score: 154.00 Matches: 26
Percent Similarity: 62.00%
Best Local Similarity: 52.00%
Query Match: 20.48%
DB: 2

US-10-006-252A-19 (1-414) x S66221 (1-50)

Qy 106 AAGTTGTGCGAAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCAATGC 165
Db 1 GluLeuCysGluLysAlaSerLysThrTrpSerGlyAsnCysGlyAsnThrGlyHisCys 20
Qy 166 AAGAATCAGTCGATTAACTTCAGAAAGCAGACATGCATCTTCCAACTATGCTTCCCA 225
Db 21 AspAsnGlnCysLysSerTrpGluGlyAlaAlaHisGlyAlaCysHisValArgAsnGly 40
Qy 226 GCTCACAGTGTATCTGCTACTTCTTGT 255
Db 41 LysHisMetCysPheCysTyrPheAsnCys 50

RESULT 15

S28993
antifungal protein 1 - white mustard (fragment)
C;Species: Sinapis alba (white mustard)
C;Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C;Accession: S28993
R;Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue,
FEBS Lett. 316, 233-240, 1993
A;Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
A;Reference number: S28989; MUID:93138130; PMID:8422949
A;Accession: S28993
A;Molecule type: protein
A;Residues: 1-25 <TER>
C;Superfamily: gamma-thionin

Alignment Scores:

Pred. No.: 6.39e-08 Length: 25
Score: 151.00 Matches: 25
Percent Similarity: 100.00%
Conservative: 0

Best Local Similarity: 100.00%
Query Match: 20.08%
DB: 2
US-10-006-252A-19 (1-414) x S28993 (1-25)

Qy 103 CAGAACTTGTGCGAAGGCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnSerAsnAla 20
Qy 163 TGCAGAAATCAGTCG 177
Db 21 CysLysAsnGlnCys 25

Search completed: May 11, 2004, 17:05:18
Job time : 19.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:57:50 ; Search time 14 Seconds
(without alignments)
3079.578 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 752
Sequence: 1 gttttattgtagcatggc.....caaaaaaaaaaaaaaaaaaaaaa 414

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p model -DEV=xlp
-Q/cn2_1/USPTO_spool_p/US10006252/runat_11052004_141657_22786/app_query.fasta_1.583
-DB=SwissProt_42 -Qfmt=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START1=END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=500 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-CUTFWT=PTC -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252 @CN 1 1 16 @runat_11052004_141657_22786 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMECUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	58.8	80	1 APP1_BRANA	P30225 brassica na
2	417	55.5	80	1 APP2_BRANA	P30230 raphanus sa
3	405	53.9	80	1 APP4_RAPSA	O24331 raphanus sa
4	403	53.6	80	1 APP4_ARATH	Q91123 arabidopsis
5	400	53.2	80	1 APP3_ARATH	O80994 arabidopsis
6	399	53.1	80	1 APP2_ARATH	O80995 arabidopsis
7	397	52.8	80	1 APP1_ARATH	P30224 arabidopsis
8	394.5	52.5	79	1 APP3_BRANA	Q39313 brassica na
9	393.5	52.3	79	1 APP3_RAPSA	O24332 raphanus sa
10	309	44.1	51	1 APP1_SINAL	P30231 sinapis alb
11	303	40.3	51	1 APP2_SINAL	P30232 sinapis alb
12	233.5	31.1	52	1 APP2_SINAL	Q10989 sinapis alb
13	161	21.4	27	1 APP1_BRANA	P22357 helianthus
14	149	19.8	161	1 APP1_HELAN	P22357 helianthus
15	142	18.9	27	1 APP2_BRANA	P30228 brassica ra
16	137	18.2	23	1 APP2_BRANA	P30226 brassica na
17	131.5	17.5	106	1 THG1_NICPA	O24115 nicotiana p
18	114	15.2	105	1 THGP_TOBAC	P30226 nicotiana t

19	109	14.5	75	1 DEF1_CAPAN	Q43413 capsicum an
20	99	13.2	73	1 THG4_ARATH	Q92ul8 arabidopsis
21	95	12.6	75	1 10KD_VIGUN	P18646 vigna ungui
22	93.5	12.4	74	1 DR39_PEA	Q01784 pisum sativ
23	87.5	11.6	72	1 D230_PEA	Q01783 pisum sativ
24	87.5	11.6	73	1 AD02_MOUSE	Q8C718 mus musculu
25	83	11.0	77	1 THG3_ARATH	Q92ul7 arabidopsis
26	82	10.9	77	1 THG1_ARATH	Q39182 arabidopsis
27	81	10.8	74	1 DEF2_CAPAN	O65740 capsicum an
28	80	10.6	46	1 AX2_ETIVU	P82010 beta vulgar
29	80	10.6	46	1 PSD1_PEA	P81929 pisum sativ
30	80	10.6	77	1 THG2_ARATH	Q1914 arabidopsis
31	80	10.6	83	1 DL_DROME	P10041 drosophila
32	79	10.5	768	1 LEM3_RAT	P98106 rattus norv
33	78.5	10.4	52	1 DEF2_SPIOL	P81571 spinacia ol
34	78	10.4	78	1 THGF_HELAN	P82659 helianthus
35	77	10.2	121	1 ASP2_HELAN	P22184 helianthus
36	77	10.2	2531	1 NTC1_RAT	Q07008 rattus norv
37	76.5	10.2	47	1 PSD2_PEA	P81930 pisum sativ
38	75.5	10.0	1389	1 LTB3_MOUSE	Q8C918 mus musculu
39	75.5	10.0	1713	1 LTB1_MOUSE	Q8C919 mus musculu
40	75	10.0	74	1 P322_SOLTU	P20346 solanum tub
41	74.5	9.9	1429	1 L112_CAEEL	P14585 caenorhabdi
42	74.5	9.9	2911	1 FBN2_HUMAN	P35556 homo sapien
43	74	9.8	1408	1 SEER_DROME	P18168 drosophila
44	73.5	9.8	313	1 COXT_KLJLA	P78990 kluyveromyc
45	73.5	9.8	1213	1 JAG3_BRARE	Q90y54 brachydanio

ALIGNMENTS

RESULT 1

ID	APP1_BRANA	STANDARD	PRT	80 AA
AC	P30225; Q41163;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DB	Cysteine-rich antifungal protein 1 precursor (APPL1).			
GN	APPL1.			
OS	Brassica napus (Rape), and			
OS	Raphanus sativus (Radish).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Brassica.			
OX	NCBI_TaxID=3708, 3726;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Brassica; STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;			
RC	MEDLINE=95299350; PubMed=7780308;			
RA	Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,			
RA	Kester A., Rees S.B., Torrekens S., Van Leuven F., Vanderleyden J.,			
RA	Cammue B.P.A., Broekaert W.F.;			
RA	"Small cysteine-rich antifungal proteins from radish: their role in			
RT	host defense."			
RL	Plant Cell 7:568-573 (1995).			
RN	[2]			
RP	SEQUENCE OF 30-73.			
RC	SPECIES=Brassica; TISSUE=Seed;			
RC	MEDLINE=93138130; PubMed=8422949;			
RA	Terras F.R.G., Torrekens S., Van Leuven F., Osborn R.W.,			
RA	Vanderleyden J., Cammue B.P.A., Broekaert W.F.;			
RA	"A new family of basic cysteine-rich plant antifungal proteins from			
RT	Brassicaceae species."			
RL	FEBS Lett. 316:233-240 (1993).			
RN	[3]			
RP	SEQUENCE OF 30-73.			
RC	SPECIES=R. sativus; TISSUE=Seed;			
RC	MEDLINE=92348373; PubMed=1639777;			
RA	Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,			
RA	Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;			
RA	"Analysis of two novel classes of plant antifungal proteins from			
RT	radish (Raphanus sativus L.) seeds."			


```

RL J. Biol. Chem. 267:15301-15309(1992).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations.
CC -!- SUBUNIT: Forms oligomers in its native state.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U18557; AAA69541.1; -
CC PIR; T10176; T10176.
CC HSSP; P30231; LAYV.
CC InterPro; IPR008176; Gamma-thionin.
CC Pfam; PF00304; Gamma-thionin; 1.
CC ProDom; PD002594; G_Purothionin; 1.
CC SMART; SM00505; Knot1; 1.
CC PROSITE; PS00940; GAMMA_THIONIN; 1.
CC Plant defense; Fungicide; Signal; Multigene family;
CC Pyrolidone carboxylic acid.
CC SIGNAL 1 29
CC CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
CC MOD RES 30 30 PYROLIDONE CARBOXYLIC ACID.
CC DISULFID 33 80 BY SIMILARITY.
CC DISULFID 44 65 BY SIMILARITY.
CC DISULFID 50 74 BY SIMILARITY.
CC DISULFID 54 76 BY SIMILARITY.
CC SEQUENCE 80 AA; 8734 MW; 05B90FAAC8DA6C2B CRC64;

Alignment Scores:
Pred. No.: 7,46e-41 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x AFPI1_BRANA (1-80)

Qy 16 ATGGCTAAGTTGGCTGCATCATCGCACTTTCTTCTGCTCTCTTTCTTTCTGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20

Qy 76 TTCGAAGCACCAACATGTTGGAAGCAGAGAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40

Qy 136 TCAGGAGTCTGTGGAACAATAACGATCGCAAGATCAGTGCATTAACCTTGAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60

Qy 196 CGACATGATCTTGAACATATGTTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
Db 61 ArgHisGlySerCysAsnTy-ValPheProAlaHisLysCysIleCysTyPheProCys 80

RESULT 2
APP2_RAPSA STANDARD; PRT; 80 AA.
ID APP2_RAPSA
AC P30230;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2 precursor (APP2).
GN APP2.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

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CC eurosids II; Brassicales; Brassicaceae; Raphanus.
CC NCBI_TaxID=3726;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
CC MEDLINE=9599350; PubMed=7780308;
CC Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,
CC Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J.,
CC Cammue B.P.A., Broekaert W.F.;
CC "Small cysteine-rich antifungal proteins from radish: their role in
CC host defense.";
CC Plant Cell 7:573-588(1995).
CC [2]
CC SEQUENCE OF 30-65.
CC TISSUE=Seed;
CC MEDLINE=92348373; PubMed=1639777;
CC Terras F.R.G., Schoofs H.M.E., de Bolle M.P.C., van Leuven F.,
CC Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
CC "Analysis of two novel classes of plant antifungal proteins from
CC radish (Raphanus sativus L.) seeds.";
CC J. Biol. Chem. 267:15301-15309(1992).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U18556; AAA69540.1; -
CC PIR; T10823; T10823.
CC HSSP; P30231; LAYV.
CC InterPro; IPR008176; Gamma-thionin.
CC Pfam; PF00304; Gamma-thionin; 1.
CC ProDom; PD002594; G_Purothionin; 1.
CC SMART; SM00505; Knot1; 1.
CC PROSITE; PS00940; GAMMA_THIONIN; 1.
CC Plant defense; Fungicide; Signal; Multigene family;
CC Pyrolidone carboxylic acid.
CC SIGNAL 1 29
CC CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 2.
CC MOD RES 30 30 PYROLIDONE CARBOXYLIC ACID.
CC DISULFID 33 80 BY SIMILARITY.
CC DISULFID 44 65 BY SIMILARITY.
CC DISULFID 50 74 BY SIMILARITY.
CC DISULFID 54 76 BY SIMILARITY.
CC SEQUENCE 80 AA; 8875 MW; 746110D9A8CE6370 CRC64;

Alignment Scores:
Pred. No.: 4,36e-38 Length: 80
Score: 417.00 Matches: 74
Percent Similarity: 95.00% Conservative: 2
Best Local Similarity: 92.50% Mismatches: 4
Query Match: 55.45% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x APP2_RAPSA (1-80)

Qy 16 ATGGCTAAGTTGGCTGCATCATCGCACTTTCTTCTGCTCTCTTTCTTTCTGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20

Qy 76 TTCGAAGCACCAACATGTTGGAAGCAGAGAGTTGTGCGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40

Qy 136 TCAGGAGTCTGTGGAACAATAACGATCGCAAGATCAGTGCATTAACCTTGAGAAGCA 195

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Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyzValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3
APP4_RAPSA
ID APP4_RAPSA STANDARD; PRT; 80 AA.
AC Q2433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 4 precursor (APP4).
GN APP4.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the plant defensin family.
CC
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CC
CC EMBL; X97318; CAA65983.1; -.
CC FR; T10183; T10183.
CC HSP; P30231; IAYU.
CC InterPro; IPR008176; Gamma-thionin.
CC Pfam; PF003614; Knot1.
CC ProDom; PD002594; G_Purothionin; 1.
CC SMART; SM00505; Knot1; 1.
CC PROSITE; PS00940; GAMMA_THIONIN; 1.
CC Plant defense; Fungicide; Signal; Multigene family;
CC Pyrrolidone carboxylic acid.
CC SIGNAL 1 29 POTENTIAL.
CC CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 4.
CC MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC FT DISULFID 33 80 BY SIMILARITY.
CC FT DISULFID 44 65 BY SIMILARITY.
CC FT DISULFID 54 76 BY SIMILARITY.
CC SQ SEQUENCE 80 AA; 8873 MW; B5F667B6441818C9 CRC64;

Alignment Scores:
Pred. No.: 9,26e-37 Length: 80
Score: 405.00 Matches: 72
Percent Similarity: 92.50% Conservative: 2
Best Local Similarity: 90.00% Mismatches: 6
Query Match: 53.86% Indels: 0
DB: 1 Gaps: 0

US-10-006-252a-19 (1-414) x APP4_RAPSA (1-80)

QY 16 ATGGCTAAGTTGCTCCATCATCGCACTTCTTTGCTGCTTGTCTTTGCTGCT 75

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Db 1 MetAlaLysPheValSerIleIleThrLeuLeuPheValAlaLeuValLeuPheAlaLa 20
QY 76 TTCGAAGCCCAACAATAGTGTGAAGCACAGAAAGTTGTGCGAAGGCCAAGTGGACATGG 135
Db PheGluAlaProThrValGluAlaGlnLysLeuCysGluArgSerSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTCGAACAATAACCGATCGACAGATCAGTCATTAACTTCAGAGAACA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
QY 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyzValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 4
APP4_ARATH
ID APP4_ARATH STANDARD; PRT; 80 AA.
AC Q9P123; P82786;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cysteine-rich antifungal protein LCR77 precursor (APP).
GN LCR77 OR AT5G44420 OR MFC16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99397451; PubMed=10470850;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
RT Sequence features of the regions of 1,011,550 bp covered by seventeen
RT P1 and TAC clones.";
RNA Res. 6:183-195(1999).
RN [2]
RP IDENTIFICATION.
RA Vancosthuyse V., Mieg C., Dumas C., Cock J.M.;
RL Submitted (JUN-2000) to Swiss-Prot.
CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the plant defensin family.
CC
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CC
CC EMBL; AB017065; BAB09149.1; -.
CC HSP; P30231; IAYU.
CC InterPro; IPR008176; Gamma-thionin.
CC Pfam; PF003614; Knot1.
CC ProDom; PD002594; G_Purothionin; 1.
CC SMART; SM00505; Knot1; 1.
CC PROSITE; PS00940; GAMMA_THIONIN; 1.
CC Plant defense; Fungicide; Signal; Multigene family;
CC Pyrrolidone carboxylic acid.
CC SIGNAL 1 29 POTENTIAL.
CC CHAIN 30 80 PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
CC LCR77.
CC MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC FT DISULFID 33 80 BY SIMILARITY.
CC FT DISULFID 44 65 BY SIMILARITY.
CC FT DISULFID 50 74 BY SIMILARITY.

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FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8518 MW; 2D0DAFB38E9B6321 CRC64;

Alignment Scores:
Pred. No.: 1 54e-36 Length: 80
Score: 403.00 Matches: 71
Percent Similarity: 95.00% Conservative: 5
Best Local Similarity: 88.75% Mismatches: 4
Query Match: 53.59% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x APP4_ARATH (1-80)

QY 16 ATGGCTAAGTTTCGTCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleThrLeuIlePheAlaLeuValLeuPheAlaAla 20

QY 76 TTCGAAGCACCACAAATGCTGGAAGCAGACAGATGTTGCGAAGCCCAAGTGGACATGG 135
Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTyr 40

QY 136 TCAGGAGTCTGTGGAAACAAATACCGATCGCATGATCATGATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60

QY 196 CGACATGGATCTTGCACATGATCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 5
APP3_ARATH STANDARD; PRT; 80 AA.
AC O80954;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cysteine-rich antifungal protein At2g26020 precursor (AFP).
GN AT2g26020 OR T19L18.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
RX NCBI_TaxID=3702;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the plant defensin family.

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CC EMBL; AC004747; AAC31244.1; -.
DR PIR; T02621; T02621.

HSP: P30231; IAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G-Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 80 PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
AT2G26020.
FT MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8640 MW; 81B106058BAFFC7 CRC64;

Alignment Scores:
Pred. No.: 3 31e-36 Length: 80
Score: 400.00 Matches: 70
Percent Similarity: 93.75% Conservative: 5
Best Local Similarity: 87.50% Mismatches: 5
Query Match: 53.19% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x APP3_ARATH (1-80)

QY 16 ATGGCTAAGTTTCGTCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleThrLeuIlePheAlaLeuValLeuPheAlaAla 20

QY 76 TTCGAAGCACCACAAATGCTGGAAGCAGACAGATGTTGCGAAGCCCAAGTGGACATGG 135
Db 21 PheGluValProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTyr 40

QY 136 TCAGGAGTCTGTGGAAACAAATACCGATCGCATGATCATGATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60

QY 196 CGACATGGATCTTGCACATGATCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 6
APP2_ARATH STANDARD; PRT; 80 AA.
ID APP2_ARATH
AC O80955; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cysteine-rich antifungal protein At2g26010 precursor (AFP).
GN AT2g26010 OR T19L18.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
RX NCBI_TaxID=3702;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the plant defensin family.

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CC EMBL; AC004747; AAC31244.1; -.
DR PIR; T02621; T02621.

RT thaliana.";
 RL Nature 402:761-768(1999).
 CC -|- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations (By similarity).
 CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -|- SIMILARITY: Belongs to the plant defensin family.
 CC
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 CC
 CC EMBL; AC004747; AAC31234.1; -.
 DR PIR; T02622; T02622.
 DR HSP; P30231; 1A9V.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knott.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G.Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 KW Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 80
 FT
 FT MOD_RES 30 30
 FT
 FT DISULFID 33 80
 FT DISULFID 44 65
 FT DISULFID 50 74
 FT DISULFID 54 76
 FT
 FT SEQUENCE 80 AA; 8580 MW; 99E1E0D4443AD67B CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 4.27e-36 Length: 80
 Scores: 399.00 Matches: 71
 Percent Similarity: 93.75% Conservative: 4
 Best Local Similarity: 88.75% Mismatches: 5
 Query Match: 53.06% Indels: 0
 DB: 1 Gaps: 0
 US-10-006-252a-19 (1-414) x AFP2_ARATH (1-80)
 Qy 16 ATGGCTAAGTTGGTCCATCATCGACATCTTTTTCGCTGCTGCTTTTCTGCTGCT 75
 Db 1 MetAlalysSerAlaAlaIlelleThrPheLeuPheAlaLeuValLeuPheAlaala 20
 Qy 76 TTGAGCACCAACAATGGTGGAGCACAGAGTTGTGGCAAGGCAAGTGGGACATGG 135
 Db 21 PheGluAlaProIleMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 Qy 136 TCAGGAGTCGTGGACACATACCGATCATCAGATCATGATGATTAACCTTGAGAAACA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 Qy 196 CGATCATGATTTGCAACTATGCTTTCCAGCTCACAAGTGTATGCTGCTTCTCTGT 255
 Db 61 LysHisGlySerCysAsnTrpValPheProAlaHisLysCysIleCysTrpPheProCys 80
 RESULT 7
 APPL_ARATH
 ID APPL_ARATH STANDARD; PRT; 80 AA.
 AC P30224; Q42179;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 precursor (APPL) (Anther-specific
 DE protein S18 homolog).
 GN APPL1 OR PDF1.1 OR AT1G75830 OR T4012.6 OR T4012.7.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Raynal M., Grellert F., Laudie M., Meyer Y., Cooke R., Delseny M.,
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Seed;
 RA Raynal M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=99178804; PubMed=10080719;
 RA Williams R.W., Clark S.E., Meyerowitz E.M.;
 RT "Genetic and physical characterization of a region of Arabidopsis
 RL chromosome 1 containing the CLAVATA1 gene.";
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buchler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Dunn P., Etny P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.S., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambling G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RL thaliana.";
 RN Nature 408:816-820(2000).
 RN [5]
 RP SEQUENCE OF 30-56.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.P.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RL Brassicaceae species.";
 CC FEBS Lett. 316:233-240(1993).
 CC -|- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -|- SUBUNIT: Forms oligomers in its native state.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- SIMILARITY: Belongs to the plant defensin family.
 CC
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 CC
 CC EMBL; Z27258; CAA81770.1; -.
 DR EMBL; Z29957; CAA82845.1; -.
 DR EMBL; X91916; CAA63009.1; -.
 DR EMBL; AF049870; AAD02502.1; -.
 DR EMBL; AC007396; AAF26754.1; -.

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EMBL; U59459; RA003224.1; -
 PIR; T07917; T07917.
 HSSP; P30231; IAYJ.
 InterPro; IPR008176; Gamma-thionin.
 InterPro; IPR003614; Kncoti.
 Pfam; PF00304; Gamma-thionin; 1.
 ProDom; PD002594; G_Purothionin; 1.
 SMART; SM00505; Kncoti; 1.
 PROSITE; PS00940; GAMMA_THIONIN; 1.
 Plant defense; Fungicide; Signal; Multigene family.
 SIGNAL 1 29
 CHAIN 30 79
 DISULFID 32 79
 DISULFID 43 64
 DISULFID 49 73
 DISULFID 53 75
 CONFLICT 33 76
 SEQUENCE 80 AA; 8709 MW; 99F34A8DA360441F CRC64;

Alignment Scores:
 Pred. No.: 1 34e-35 Length: 79
 Score: 397.00 Matches: 70
 Percent Similarity: 92.50% Conservative: 4
 Best Local Similarity: 87.50% Mismatches: 6
 Query Match: 52.79% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x APP1_ARATH (1-80)
 QY 16 ATGGCTAAGTTTGCGTCATCATCGACCTCTTTTGTCTGCTCTTTTGTCTGCTGCT 75
 Db 1 MetAlaLysSerAlaThrIleValThrLeuPhePheAlaAlaLeuValPhePheAlaAla 20
 QY 76 TTCGAGCACCACCAATGCTGGAGACACAGAGTGTGGCAAGCGCAGTGGGACATGG 135
 Db 21 LeuGluAlaProMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGAGTCTGTGAAACAATAACGATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGAGCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
 Db 61 ArgHisGlySerCysAsnTyrrValPheProAlaHisLysCysIleCysTyrrPheProCys 80

RESULT 8
 APP3_BRANA
 ID APP3_BRANA STANDARD; PRT; 79 AA.
 AC Q39313;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 3 precursor (APP3).
 GN APP3.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 NCBI_TaxID=3708;
 RN [1]
 RX SEQUENCE FROM N.A.
 RC STRAIN=cnv. Naehaen;
 RA Sohn U., Lee C.M., Lee M.H., Kim J.H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 cations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the plant defensin family.

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DR EMBL; X97319; CAA65984.1; --
 DR PIR; T10243; T10243.
 DR HSSP; P30231; LAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA-THIONIN; 1.
 DR Plant defense; Fungicide; Signal; Multigene family.
 KW SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 79
 FT DISULFID 32 79 CYS-STEINE-RICH ANTIFUNGAL PROTEIN 3.
 FT DISULFID 43 64 BY SIMILARITY.
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 75 BY SIMILARITY.
 SQ SEQUENCE 79 AA; 8479 MW; BAPFA80465DB48548 CRC64;

Alignment Scores:
 Pred. No.: 1,73e-35 Length: 79
 Score: 395.50 Matches: 72
 Percent Similarity: 95.00% Conservative: 4
 Best Local Similarity: 90.00% Mismatches: 3
 Query Match: 52.33% Indels: 1
 DB: 1 Gaps: 1

US-10-006-252A-19 (1-414) x APP3_RAPSA (1-79)

QY 16 ATGGCTAAGTTTGGTCATCATCGCACTCTTTTGGCTCTTGTCTTTTCTGCTGCT 75
 Db 1 MetAlalysPheAlaSerIleValAlaLeuPheAlaLeuValPheAlaAla 20
 QY 76 TTCGAGCACCACATGTTGGGAGCACAGAGTTGTGGGAAAGCCAGTGGGACATGG 135
 Db 21 PheGluAlaProThrValValGluAla---LysLeuCysGluArgSerSerGlyThrTrp 39
 QY 136 TCAGGAGCTCTGTGGAACATATAACGCATCGAAGATCAGTGCATTAACTTTCGAGAAAGCA 195
 Db 40 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 59
 QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTATCTGCTACTTCTTCTGT 255
 Db 60 GlnHisGlySerCysAsnTyValPheProAlaHisLysCysIleCysTy-PheProCys 79

RESULT 10
 AFPI_SINAL
 ID_AFPI_SINAL STANDARD; PRT; 51 AA.
 AC P30231;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 (AFPI) (M1).
 OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed.
 RX MEDLINE=86433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;
 RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as

RT antifungal proteins.";
 RL Int. J. Pept. Protein Res. 47:437-446(1996).
 RN [2]
 RP SEQUENCE OF 1-25.
 RC TISSUE=Seed;
 RX MEDLINE=931138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98300344; PubMed=9636715;
 RA Fant F., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
 RT "Determination of the three-dimensional solution structure of Raphanus
 RT sativus antifungal protein 1 by 1H NMR.";
 RL J. Mol. Biol. 279:257-270(1998).
 CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -1- SUBUNIT: Forms oligomers in its native state.
 CC -1- MASS SPECTROMETRY: MW=5677; MW_ERR=1.0; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 DR PDB; LAYJ; 28-JAN-98.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA-THIONIN; 1.
 KW Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 4 51
 FT DISULFID 15 36
 FT DISULFID 21 45
 FT DISULFID 25 47
 FT STRAND 4 7
 FT HELIX 18 28
 FT STRAND 34 37
 FT STRAND 44 49
 SQ SEQUENCE 51 AA; 5695 MW; 770990E72DD1C469 CRC64;

Alignment Scores:
 Pred. No.: 3,75e-26 Length: 51
 Score: 309.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 41.09% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x AFPI_SINAL (1-51)

QY 103 CAGAGCTTGGGAGCCAGTGGACATGCTCAGGAGTCTGTGGAAAACAATAAGCA 162
 Db 1 GlnHisLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGATCAGTGCATTAACTTCAGAAAGCACACATGGATCTTGCAACTGTCTTC 222
 Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyValPhe 40
 QY 223 CGAGCTCACAAGTATCTGCTACTTCTTCTGT 255
 Db 41 ProAlaHisLysCysIleCysTy-PheProCys 51

RESULT 11
 AF2A_SINAL
 ID_AF2A_SINAL STANDARD; PRT; 51 AA.
 AC P30232;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2A (AF2A) (M2A).
 OS Sinapis alba (White mustard) (Brassica hirta).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;
 RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RT antifungal proteins.";
 RL Int. J. Pept. Protein Res. 47:437-446(1996).
 RN [2]
 RP SEQUENCE OF 1-26.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leeuwen F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- MASS SPECTROMETRY: MW=5705; MW ERR=0.8; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR HSP; P30231; 1AUV.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Klot1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G. Purothionin; 1.
 DR SMART: SM00505; Klot1; 1.
 DR PROSITE: PS00940; GAMMA THIONIN; 1.
 DR Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
 FT DISULFID 4 52 BY SIMILARITY.
 FT DISULFID 15 36 BY SIMILARITY.
 FT DISULFID 21 45 BY SIMILARITY.
 FT DISULFID 25 47 BY SIMILARITY.
 SQ SEQUENCE 51 AA; 5722 MW; 1C7F50E72DC945B1 CRC64;

Alignment Scores:

Pred. No.: 1.73e-25 Length: 51
 Score: 303.00 Matches: 49
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 96.08% Mismatches: 0
 Query Match: 40.29% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252a-19 (1-414) x AF2A_SINAL (1-51)

QY 103 CAGAGTTGTCGGAAGCCAGTGGACATGTCAGGAGTGTGGAAACAAATACGCA 162
 Db 1 GlnLysLeuCysGlnAArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGATCATGTCATTAACTTGCAGACGACGATGCTTGCACACTATGCTTC 222
 Db 21 CysArgAsnGlnCysIleAsnLeuGluLeuGluLeuGluLeuGluLeuGluLeuValPhe 40
 QY 223 CAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
 Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 12

AF2B_SINAL
 ID AF2B_SINAL STANDARD; PRT; 52 AA.
 AC Q10989;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2B (APP2B) (M2B).

OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;
 RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RT antifungal proteins.";
 RL Int. J. Pept. Protein Res. 47:437-446(1996).
 RN [2]
 RP SEQUENCE OF 1-26.
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- MASS SPECTROMETRY: MW=5840; MW ERR=1.2; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR HSP; P30231; 1AUV.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Klot1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G. Purothionin; 1.
 DR SMART: SM00505; Klot1; 1.
 DR PROSITE: PS00940; GAMMA THIONIN; FALSE NEG.
 KW Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
 FT DISULFID 4 52 BY SIMILARITY.
 FT DISULFID 16 37 BY SIMILARITY.
 FT DISULFID 22 46 BY SIMILARITY.
 FT DISULFID 26 48 BY SIMILARITY.
 SQ SEQUENCE 52 AA; 5856 MW; A060FCBC13A8D1FB CRC64;

Alignment Scores:

Pred. No.: 8.48e-18 Length: 52
 Score: 233.50 Matches: 40
 Percent Similarity: 84.62% Conservative: 4
 Best Local Similarity: 76.92% Mismatches: 7
 Query Match: 31.05% Indels: 1
 DB: 1 Gaps: 1

US-10-006-252a-19 (1-414) x AF2B_SINAL (1-52)

QY 103 CAGAGTTGTCGGAAGCCAGTGGACATG---TCAGAGTCTGTGGAACAAATAC 159
 Db 1 GlnLysLeuCysAlaArgProSerGlyThrTrpSerGlyAsnCysArgAsnAsn 20
 QY 160 GCATGCAAGATCATGTCATTAACTTGCAGACGACGATGCTTGCACACTATGTC 219
 Db 21 AlaCysArgAsnPheCysIleLysLeuGluLysSerArgHisGlySerCysAsnIlePro 40
 QY 220 TTCGAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
 Db 41 PheProSerAsnLysCysIleCysTyrPheProCys 52

RESULT 13

AFPI_BRARA
 ID AFPI_BRARA STANDARD; PRT; 27 AA.
 AC P30227;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 (APPI) (Fragment).

OS Brassica rapa (Turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=51350;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;

RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -1- SUBUNIT: Forms oligomers in its native state.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 CC HSP; S28989; S28989.
 DR PIR; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2925 MW; 4C85BD9C611D4A9E CRC64;
 Alignment Scores:
 Pred. No.: 8.5e-10 Length: 27
 Score: 161.00 Matches: 27
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.41% Indels: 0
 DB: 0 Gaps: 0
 US-10-006-252A-19 (1-414) x APPI_BRARA (1-27)
 QY 103 CAGAAGTTGCGAAGCCAAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGAAATCACTGCAATTAAC 183
 Db 21 CysLysAsnGlnCysIleAsn 27
 RESULT 14
 ASFL_HELAN
 ID _APP2_BRARA STANDARD; PRT; 161 AA.
 AC P22357;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Anther-specific protein SF18 precursor (Fragment).
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
 OC Helianthus.
 OC NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. HA401B / Cargill; TISSUE=Anther;
 RX MEDLINE=91338702; PubMed=2102380;
 RA Domon C., Evrard J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;
 RT "Nucleotide sequence of two anther-specific cDNAs from sunflower
 RL (Helianthus annuus L.).";
 RL Plant Mol. Biol. 15:643-646(1990).
 CC -1- FUNCTION: Anther-specific cell wall protein which could contribute
 CC to the cell wall architecture of epidermal anther cells via
 CC intermolecular disulfide bridges.
 CC -1- TISSUE SPECIFICITY: Epidermal anther cells.
 CC -1- DEVELOPMENTAL STAGE: Late developmental stages.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch.
 CC EMBL; X53375; CAA37455.1; -.
 DR PIR; S12246; S12246.
 DR HSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Signal; Cell wall.
 FT NON_TER 1 1
 FT SIGNAL <1 8
 FT CHAIN 9 161 ANTER-SPECIFIC PROTEIN SF18.
 FT DOMAIN 9 65 GAMMA-THIONIN LIKE DOMAIN.
 FT DOMAIN 70 161 PROLINE DOMAIN.
 FT DISULFID 18 65 BY SIMILARITY.
 FT DISULFID 29 50 BY SIMILARITY.
 FT DISULFID 35 59 BY SIMILARITY.
 FT DISULFID 39 61 BY SIMILARITY.
 SQ SEQUENCE 161 AA; 15363 MW; 27A9CF4633ADA02B CRC64;
 Alignment Scores:
 Pred. No.: 2.06e-08 Length: 161
 Score: 149.00 Matches: 23
 Percent Similarity: 64.00% Conservative: 9
 Best Local Similarity: 46.00% Mismatches: 18
 Query Match: 19.81% Indels: 0
 DB: 1 Gaps: 0
 US-10-006-252A-19 (1-414) x ASFL_HELAN (1-161)
 QY 106 AGCTTGTGCGAAGCCAAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGCAATGC 165
 Db 16 LysLeuCysGlnLysProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 166 AAGAATCACTGCAATTAACCTTGGAGAAAGCACACATGTCAGGAGTCTGTGCAACTGTCTTCCCA 225
 Db 36 AspLysArgCysIleAsnTrpGluGlyAlaLysHisGlyAlaCysHisGlnArgGluAla 55
 QY 226 GCTCACAAGTGTATCTGCTACTTCTCTGT 255
 Db 56 LysHisMetCysPheCysTyrPheAspCys 65
 RESULT 15
 APP2_BRARA
 ID _APP2_BRARA STANDARD; PRT; 27 AA.
 AC P30238;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2 (APP2) (Fragment).
 OS Brassica rapa (Turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=51350;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RL Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -1- FUNCTION: Possesses some antifungal activity sensitive to
 CC inorganic cations and antibacterial activity against B.megaterium.
 CC -1- SUBUNIT: Forms oligomers in its native state.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 DR PIR; S28990; S28990.
 DR HSP; P30231; IAYJ.

DR InterPro: IPR008176; Gamma-thionin.
 DR ProDom: PD002594; Gamma-thionin; 1.
 DR PROSITE: PS00940; GAMMA-THIONIN; 1.
 KW Plant defense; Fungicide; Antibiotic; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT UNSURE 27 27
 FT NON TER 27 27
 SQ SEQUENCE 27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;

Alignment Scores:
 Pred. No.: 1.07e-07 Length: 27
 Score: 142.00 Matches: 25
 Percent Similarity: 96.15% Conservative: 0
 Best Local Similarity: 96.15% Mismatches: 1
 Query Match: 18.88% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) X APP2_BRARA (1-27)

Qy	103	CAGAGTTTGTGGAAAGCCAGTGGACATGTCAGGAGTCTGTGGAACATAACGCA	162
Db	1	GlnLysLeuCysGluArgProSerGlyThr***SerGlyValCysGlyAsnAsnAla	20
Qy	163	TGCAGAAATCAGTGCAAT	180
Db	21	CysLysAsnGlnCysIle	26

Search completed: May 11, 2004, 17:03:07
 Job time : 29 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:58:28 ; Search time 41 seconds

(without alignments)

6371.929 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

Sequence: 1 gttttattgtatcatggc.....caaaaaaaaaaaaaaaaaaaaa 414

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DBV=slp
-Q=/cgn2_1/USPTO.spool_p/US10006252/runat_11052004_141657_22797/app.query.fasta_1.583
-DB=SPTRMBL 25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NCRM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252@cgn_1_1_86/runat_11052004_141657_22797 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL 25:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_virus:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	421	56.0	80	10	Q94IN7

	2	407	54.1	80	10	Q9FS38
	3	402	53.5	80	10	Q8H6K0
	4	398	52.9	80	10	Q9FI22
	5	207	27.5	80	10	Q9FZ31
	6	181	24.1	78	10	Q8VQ7
	7	164	21.8	56	10	Q9FWR6
	8	153.5	20.4	108	10	Q8LSM8
	9	141.5	18.8	105	10	Q40128
	10	139.5	18.6	132	10	Q842X5
	11	118	15.7	83	10	Q8GTL2
	12	116	15.4	105	10	Q8GTM0
	13	115	15.3	83	10	Q40779
	14	114	15.2	105	10	Q24105
	15	112	14.9	75	10	Q8W434
	16	110.5	14.7	83	10	Q40539
	17	109	14.5	101	10	Q8H600
	18	108	14.4	77	10	Q82788
	19	107.5	14.3	87	10	Q48T3
	20	103.5	13.8	81	10	Q48T2
	21	100	13.3	103	10	Q8H6Q1
	22	95.5	12.7	87	10	Q48T4
	23	94.5	12.6	107	10	Q3XHE3
	24	93.5	12.4	76	10	Q8LEG6
	25	92	12.2	108	10	Q82789
	26	91.5	12.2	81	10	Q4225
	27	90.5	12.1	380	10	Q49590
	28	86.5	11.5	72	10	Q9FR81
	29	86.5	11.5	78	10	Q8W4V6
	30	85.5	11.4	81	10	Q82756
	31	85	11.3	79	10	Q24104
	32	85	11.3	217	13	P70016
	33	82.5	11.0	76	10	P82732
	34	82.5	11.1	221	5	Q20860
	35	81.5	10.8	79	10	Q39807
	36	81	10.8	78	10	Q8MB66
	37	81	10.8	82	10	Q8L698
	38	80.5	10.7	84	10	Q8SEM4
	39	79	10.5	60	10	Q8H6L2
	40	79	10.5	77	10	Q39403
	41	79	10.5	77	10	Q24094
	42	79	10.5	794	5	Q8T4P0
	43	79	10.5	1065	11	Q810H2
	44	78.5	10.5	715	5	Q9NAP6
	45	78	10.4	88	10	Q94A28

ALIGNMENTS

RESULT 1

ID	Q94IN7	PRELIMINARY;	PRT;	80 AA.
AC	Q94IN7;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Defensin precursor.			
GN	DEF.			
OS	Brassica oleracea (Cauliflower).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Brassica.			
OX	NCBI_TaxID=3712;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Esnault R.;			
RL	"Brassica oleracea def gene for defensin.";			
RT	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ311046; CAC37558.1;			
DR	GO; GO:0003793; F:defense/immunity protein activity; IEA.			
DR	InterPro; IPR008176; Gamma-thionin.			
DR	InterPro; IPR003614; Kncn1.			
DR	Pfam; PF00304; Gamma-thionin; 1.			
DR	ProDom; PD002594; G_Purothionin; 1.			

DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW SIGNAL. 1 29 POTENTIAL
 FT SIGNAL. 1 29 POTENTIAL
 SQ SEQUENCE 80 AA; 8740 MW; 980477DFED8D2690 CRC64;

Alignment Scores:
 Pred. No.: 5.6e-41 Length: 80
 Score: 421.00 Matches: 75
 Percent Similarity: 96.25% Conservative: 2
 Best Local Similarity: 93.75% Mismatches: 3
 Query Match: 55.98% Indels: 0
 DB: 10 Gaps: 0

US-10-006-252A-19 (1-414) x Q94IN7 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTCTTTTGGCTGCT 75
 DB 1 MetAlaLysValAlaSerIleValAlaLeuPheProAlaLeuValIlePheAlaAla 20

QY 76 TTCGAAGCCACCAATGTGGAGCACAGAGTGTGGAAAGCCCAAGTGGGACATGG 135
 DB 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrrp 40

QY 136 TCAGGAGTCTGTGGAACATAACGATGCAAGATGTCAGATGCAATTAACCTTGAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60

QY 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
 DB 61 ArgHisGlySerCysAsnTyValPheProAlaHisLysCysIleCysTyPheProCys 80

RESULT 2

Q9FS38 PRELIMINARY; PRT; 80 AA.
 ID Q9FS38
 AC Q9FS38; (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMELrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Gamma-thionin precursor.
 OS Eutrema wasabi.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Eutrema.
 OX NCBI_TaxID=75806;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf, and Stem;
 RX MEDLINE=21071227; PubMed=11204773;
 RA Saitoh H., Kiba A., Nishihara M., Yamamura S., Suzuki K., Terauchi R.;
 RT "Production of antimicrobial defensin in Nicotiana benthamiana with a
 potato virus X vector";
 RL Mol. Plant Microbe Interact. 14:111-115 (2001).
 DR EMBL; AB012871; BAB19054.1; -;
 DR HSSP; P30231; IAYJ.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knott1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Signal.
 FT SIGNAL. 1 29 POTENTIAL.
 FT CHAIN. 30 80 POTENTIAL.
 SQ SEQUENCE 80 AA; 8761 MW; CF2F10ADD38FC87A CRC64;

Alignment Scores:
 Pred. No.: 2.57e-39 Length: 80
 Score: 407.00 Matches: 72
 Percent Similarity: 96.25% Conservative: 5
 Best Local Similarity: 90.00% Mismatches: 3
 Query Match: 54.12% Indels: 0

DB: 10 Gaps: 0

US-10-006-252A-19 (1-414) x Q9FS38 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTCTTTTGGCTGCT 75
 DB 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheSerAla 20

QY 76 TTCGAAGCCACCAATGTGGAGCACAGAGTGTGGAAAGCCCAAGTGGGACATGG 135
 DB 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrrp 40

QY 136 TCAGGAGTCTGTGGAACATAACGATGCAAGATGTCAGATGCAATTAACCTTGAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60

QY 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
 DB 61 ArgHisGlySerCysAsnTyIlePheProTyHisArgCysIleCysTyPheProCys 80

RESULT 3

Q8H6K0 PRELIMINARY; PRT; 80 AA.
 ID Q8H6K0
 AC Q8H6K0;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Defensin.
 OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=51351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ryang S.-H., Chung S.-Y., Park Y.-S., Cho T.-J.;
 RT "Characterization of Chinese cabbage genes induced by Pseudomonas
 syringae pv. tomato";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF528180; AAN23105.1; -;
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knott1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 SQ SEQUENCE 80 AA; 8564 MW; 485CC5A95905E92C CRC64;

Alignment Scores:
 Pred. No.: 1.01e-38 Length: 80
 Score: 402.00 Matches: 72
 Percent Similarity: 92.50% Conservative: 2
 Best Local Similarity: 90.00% Mismatches: 6
 Query Match: 53.46% Indels: 0
 DB: 10 Gaps: 0

US-10-006-252A-19 (1-414) x Q8H6K0 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTGCTTCTTTTGGCTGCT 75
 DB 1 MetAlaLysPheValSerIleIleThrLeuPhePheAlaLeuValLeuPheAlaAla 20

QY 76 TTCGAAGCCACCAATGTGGAGCACAGAGTGTGGAAAGCCCAAGTGGGACATGG 135
 DB 21 PheGluAlaProThrMetValLysAlaGlnLysLeuCysGluArgSerGlyThrTrrp 40

QY 136 TCAGGAGTCTGTGGAACATAACGATGCAAGATGTCAGATGCAATTAACCTTGAGAAAGCA 195
 DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60

QY 196 CGACATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
 DB 61 ArgHisGlySerCysAsnTyIlePheProTyHisArgCysIleCysTyPheProCys 80

Db 61 ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80
 RESULT 4
 Q9FI22
 ID Q9FI22 PRELIMINARY; PRT; 80 AA.
 AC Q9FI22
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Antifungal protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT P1 and TAC clones.";
 RL DNA Res. 6:183-195(1999).
 DR EMBL; AB017085; BAB09150.1; -.
 DR HSP; P30231; IAYJ.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA-THIONIN; 1.
 SQ SEQUENCE 80 AA; 8550 MW; 44ELF6D8452AC76E CRC64;
 Alignment Scores:
 Pred. No.: 3,01e-38 Length: 80
 Score: 398.00 Matches: 71
 Percent Similarity: 93.75% Conservative: 4
 Best Local Similarity: 88.75% Mismatches: 5
 Query Match: 52.93% Indels: 0
 DB: 10 Gaps: 0
 US-10-006-252a-19 (1-414) x Q9FI22 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 75
 Db 1 MetAlaLysSerAlaThrIleThrPheLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTGGAAGCACCAATGGGAGACACAGAGTTTGGCAAGTGGCAAGTGGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAAATACGCATGCAGATCATGCTTACCTTGGAGAACCA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTATGCTACTTCTTCTTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
 RESULT 5
 Q9FZ31
 ID Q9FZ31 PRELIMINARY; PRT; 80 AA.
 AC Q9FZ31
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative antifungal protein (Cysteine-rich antifungal protein,
 DE putative).
 DE T24C10.12 OR F14C21.57.
 OS Arabidopsis thaliana (Mouse-ear cress).
 Db 61 ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Feng J.-D., Frey T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblyum T.V., Fong B., Hansen N.F., Fujii C.Y.,
 RA Giller J.E., Goldsmith A.D., Haas B., Johnson-Hopson C., Khan S., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
 RA Miitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).
 DR EMBL; AC064840; AAG00880.1; -.
 DR EMBL; AC069144; AAG51104.1; -.
 DR PIR; P96591; F96591.
 DR HSP; P30231; IAYJ.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin; 1.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 SQ SEQUENCE 80 AA; 9139 MW; 83FBF4ACA7974071 CRC64;
 Alignment Scores:
 Pred. No.: 1.4e-15 Length: 80
 Score: 207.00 Matches: 40
 Percent Similarity: 67.90% Conservative: 15
 Best Local Similarity: 49.38% Mismatches: 24
 Query Match: 27.53% Indels: 2
 DB: 10 Gaps: 2
 US-10-006-252a-19 (1-414) x Q9FZ31 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 75
 Db 1 MetAlaLysPheCysThrThrIleThrLeuLeuValAlaLeuValLeuPheAlaAsp 20
 QY 76 TTGGAAGCACCAATGGTGGAGACACAGAGTTTGGCAAGTGGCAAGTGGGACATGG 135
 Db 21 PheGluAlaProThrIleValLysAlaGlu---LeuCysLysArgGluSerGluThrTrp 39
 QY 136 TCAGGAGTCTGTGGAAACAAATACGCATGCAGATCATGCTTACCTTGGAGAACCA 195
 Db 40 SerGlyArgCysValAsnAspThrGlnCysArgAspHisCysIleAsnAsnAspArgGly 59
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAG---TGTATCTGCTACTTCTCT 252
 Db 60 AsnAspGlyTyrCysAlaGlyGlyTyrProTrpTyrArgSerCysPheCysPhePheSer 79

Qy 253 TGT 255
Db 80 Cys 80

RESULT 6
Q8VZQ7 PRELIMINARY; PRT; 78 AA.

ID Q8VZQ7
AC Q8VZQ7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative defensin AMP1 protein.
GN Atg1g19610.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Garninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseima E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA "Full length cDNA of gene At1g19610 (GI:152233595)";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA "Arabidopsis Open Reading Frame (ORF) Clones";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN ENBL; AY063933; AL36289.1; -
DR ENBL; AY114038; RAM45086.1; -
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR PROSITE; PS00940; GAMMA THIONIN; 1.
SQ SEQUENCE 78 AA; 8840 MW; ASBDD28303A6545 CRC64;

Alignment Scores:
Pred. No.: Length: 1.7e-12 Length: 78
Score: 181.00 Matches: 31
Percent Similarity: 53.95% Conservative: 10
Best Local Similarity: 29.95% Mismatches: 35
Query Match: 40.07% Indels: 0
DB: Gaps: 0

US-10-006-252A-19 (1-414) x Q8VZQ7 (1-78)

Qy 28 GGTCATCATCGCACTTTTCTGCTCTTTTCTTTTCTGCTCTTTTCTGCAAGCACCA 87
Db 3 SerSerTyThrLeuMetLeuPheLeuCysLeuSerilePheLeuAlaSerThrGlu 22

Qy 88 ACATGGTGGAAGCAGCAAGCTTGGCAAGCCAGTGGGACAGTGCAGGACTGCT 147
Db 23 McMetAlaValGLuglyArgilecysgluargSerlysThrTrpThrGlyPheCys 42

Qy 148 GGAACAATAAACGCCATGCAAGTACATGCAATTAACTTGGAGAAACAGCATGATCT 207
Db 43 GlyAsnThrArgGlyCysAspSerGlnCyslyseArgTrpGluArgAlaSerHisglyAla 62

Qy 208 TGCACTATGCTTCCAGTCACAAAGTGTATCTGCTACTTCTTCTGT 255
Db 63 CysHisAlaGlnPheProGlyPheAlaCysPheCysTyrrPheAsnCys 78

RESULT 7
Q9FWR6 PRELIMINARY; PRT; 56 AA.

ID Q9FWR6
AC Q9FWR6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fl4Pl.6 protein.
GN Fl4Pl.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altai H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao Q., Chin C., Chiu J., Choi E., Gonzalez A.,
RA Hong B., Johnson-Hopson C., Khan S., Kim C., Koc T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharly N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.,
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN ENBL; AC024609; RAF98402.1; -
DR PIR; G86328; G86328.
DR HSP; P30231; IAY3.
DR GO; GO:0003793; P.defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; KnottI; 1.
DR PROSITE; PS00940; GAMMA THIONIN; 1.
SQ SEQUENCE 56 AA; 6403 MW; 3BD56EAA25EB0442 CRC64;

Alignment Scores:
Pred. No.: Length: 1.74e-10 Length: 56
Score: 164.00 Matches: 25
Percent Similarity: 64.00% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 18
Query Match: 21.81% Indels: 0
DB: Gaps: 0

US-10-006-252A-19 (1-414) x Q9FWR6 (1-56)

Qy 106 AAGTGTGCGAAGCCCAAGTGGAGCATGTCAGAGTCTGTGGAACAATAACGATCG 165
Db 7 ArgileCysGluArgSerLystrThrTriphrGlyPheCysGlysnThrArgGlyCys 26

Qy 166 AAGAATCAGTCATTAACTTGGAGAAAGCAGCATGATGCTTGGCAACTATGCTTCCCCA 225
Db 27 AspSerGlnCysLysArgTrpGluArgAlaSerHisGlyAlaCysHisAlaGlnPhePro 46

Qy 226 GCTCACAAGTGTATCTGCTACTTCTTCTTCTTCTTCTTCTTCTTCT 255
Db 47 GlyPheAlaCysPheCysTyrrPheAsnCys 56

RESULT 8
Q8LSM8 PRELIMINARY; PRT; 108 AA.

ID Q8LSM8
AC Q8LSM8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Defensin.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Compositae; Helianthus

[illegible]

OC Helianthus.
RN NCBI_TaxID=4232;
FX [1]
RP SEQUENCE FROM N.A.
RA Hu X., Bidney D., Duwick J., Yalpani N., Crasta O., Folkerts O.,
LA Lu G.;
ET "Oxalate oxidase confers Sclerotinia resistance";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDJF databases.
DR EMEL; AF364865; AAM27914.1; -
GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR0013614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD022594; G_Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
SQ SEQUENCE 108 AA; 11866 MW; 631ECD8F02F21AD0 CRC64;

Alignment Scores:		
Pred. No.:	Score:	
3.2e+09	Length:	108
153.50	Matches:	33
59.15%	Conservative:	9
46.48%	Mismatches:	26
20.41%	Gaps:	3
10	Indeles:	1

US-10-006-252A-19 (1-414) x Q8LSW8 (1-108)

```

QY      47 TTTTTCCTGCTTGTTGTCTTTTGGAGCACCACCATCGTGAAGCACAAGA 106
Db      11 PheLeuLeuLeuPheValLeuAlaIleSerGluleGlySer--VallysGlyGlu- 29
QY     107 AGTTGTGCAGAAAGCCCAATGGCATGTCAGAGTCTGTGGAAACAATAACGCCATGCA 166
Db      30 --LeucysGlnuylsAlaSerGlnThrTPSSrGlyThrcysGLylyThrlshisCySA 49
QY     167 AGAATCAGTGCATTACCTTTGAGAAGCACACATGATCTTGCACATTAATGCTTCCTCCAG 226
Db      49 spAspGlnCysIysSerTrpGluGlyAlaAlaHisGlyAlaCysHisValArgAspGlyL 69
QY     227 CTACAAAGTCTACTGCTACTTCCTCTGT 255
Db      69 yshlsmetCysPhecystyrPheAsnCys 78

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RESULT 9
Q40128
ID Q40128 PRELIMINARY; PRT; 105 AA.
AC Q40128
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Flower-specific gamma-thionin-like protein/acidic protein precursor.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Sreptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OX limnids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
[1]
SEQUENCE FROM N.A.
STRAIN=VF36; TISSUE=pistil;
MEDLINE=95375233; PubMed=7647301;
Milligan S.B., Gasser C.S.;
"Nature and regulation of pistil-expressed genes in tomato.";
Nature Mol. Biol. 28:691-711(1995).
EMBL; U20591; AAA80496.1; -.
PIR; S57809; S57809.
GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR008176; Gamma-thionin.
IncerPro; IPR0013614; Knot1.
Pfam; PF00304; Gamma-Thionin; 1.
ProDom; PD022594; G_Purothionin; 1.
SMART; SM00505; Knot1; 1.
SW Signal.

FT SIGNAL	1	26	POTENTIAL.
FT CHAIN	27	73	GAMMA-THIONIN-LIKE PROTEIN.
FT CHAIN	74	105	ACIDIC PROTEIN.
SQ SEQUENCE	105 AA;	11914 MW;	ADC9B7ECB620E814 CRC64;
Alignment Scores:			
Pred. No.:	8	48e-08	Length: 105
Score:	141.50	Matches:	31
Percent Similarity:	58.54%	Conservative:	17
Best local Similarity:	37.80%	Mismatches:	27
Query Match:	18.82%	Indels:	7
DB:	10	Gaps:	3
US-10-006-252A-19 (1-414) x Q40128 (1-105)			
QY	16	ATFGGTAAGTTGGTGCATCATCGCACTTCCTTTTGGCTGCTCTTCTTTTGGCTGCT	75
Db	1	MetAlaArgSerIlePhePheMetAlaPheLeuValLeuAlaMetMetLeuPheValThr	20
QY	76	TTCCGAAGCACCACACATGTTGGTGGAGACACAGAGTTGTGGAAAGGCCAAGTGGGACATGG	135
Db	21	TyrGlu-----ValGluAlaGlnGlnileCysLysAlaProSerGlnThrPhe	36
QY	136	TCAGGAGTCTGTGCAAAACAATAAGCGCATGCAAGAATCAGTGCATTAACTTTCGAGAAAGCA	195
Db	37	ProGlyLeuCysPheMetAspSerSerCysArgLysTyrCysIleLys---GluLysPhe	55
QY	196	CGACATGAGATCTTGCACATATGCTTCCAGCTCACAGTGTATCTGCTACTTTCCTTGT	255
Db	56	ThrGlyGlyHisCysSerLysLeu-----GlnArgLysCysLeuThrLysProCys	73
QY	256	TAATT 261	
Db	74	ValPhe 75	
RESULT 10			
ID	Q84ZX5	PRELIMINARY;	PRT; 132 AA.
DT	01-JUN-2003	(TrEMBLrel. 24, Created)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Major pollen allergen Art v 1 precursor.		
OS	Artemisia vulgaris (Mugwort).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	campanulids; Asterales; Asteraceae; Asteroideae; Anchemideae;		
OC	Artemisia.		
ON	NCBI_TaxID=4220;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISUUE=Pollen;		
RX	MEDLINE=22409970; PubMed=12475905;		
RA	Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N.,		
RA	Altman F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.;		
RT	Art v 1, the major allergen of mugwort pollen, is a modular		
RT	glycoprotein with a defensin-like and a hydroxyproline-rich domain.";		
RL	FASES J. 17:106-108(2003).		
DR	ENBL; AF493943; AAC04900.1;		
DR	GO; GO:0003793; P:defense/immunity protein activity; IEA.		
DR	InterPro; IPR008176; Gamma-thionin.		
DR	InterPro; IPR003614; Knot1.		
DR	PFAM; PF00304; Gamma-thionin; 1.		
DR	SMART; SM00505; Knot1; 1.		
FT SIGNAL	1	24	POTENTIAL.
FT CHAIN	25	132	MAJOR POLLEN ALLERGEN ART V 1.
SQ SEQUENCE	132 AA;	13404 MW;	745249C89919F316 CRC64;
Alignment Scores:			
Pred. No.:	1	49e-07	Length: 132
Score:	139.50	Matches:	34
Percent Similarity:	50.00%	Conservative:	10

Best Local Similarity:	38.64%	Mismatches:	25
Query Match:	18.55%	Indels:	19
DB:	10	Gaps:	5

US-10-006-252A-19 (1-414) x Q84EX5 (1-132)

QY	16	ATGGTGAAGTTTGCGTCGCATCATC---	GCACCTCTTTTTGCTGTCTGTCTTTTGTCT	72
Db	1	MetAlaLysCysSerTyrValPheCysAlaValLeuLeullePheIleValAlaIleGly	20	
QY	73	GCTTTCGAAGCACCAACAATGGTGAAGCAGCAAGTTGCGAAAGGCCAAGTCGGACA	132	
Db	21	GluMetGluAla-----	AlaGlySerLysLeuCysGluLysThrSerLysThr	36
QY	133	TGCTCAGGAGTCTGTGGAAACAATAACGCATGCAGAATCAGTGCATTAACCTTAGAAA	192	
Db	37	TyrSerGlyLysCys---AspAsnLysLysCysAspLysLysCysIleGluTrpGluLys	55	
QY	193	GCACGACATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAG-	234	
Db	56	AlaGlnHisGlyAlaCys-----	HisLysArgGluAlaGlyLysGlu	69
QY	235	---TGFATCTGCTACTTCTCTTGT	255	
Db	70	SerCysPheCysTyrPheAspCys	77	

RESULT 11

Q8GTL2 PRELIMINARY; PRT; 83 AA.

ID	Q8GTL2	PRT;	83	AA.
AC	Q8GTL2;			
DT	01-MAR-2003 (TreeBLrel. 23, Created)			
DT	01-MAR-2003 (TreeBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TreeBLrel. 25, Last annotation update)			
DE	Putative plant defensin SPILB.			
OS	Picea abies (Norway spruce) (Picea excelsa).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.			
NCHI_TaxID=3329;	[1]			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Needle;			
RA	Fossdal C.G.;			
RT	"The putative gymnosperm plant defensin (SPIL) accumulates after seed			
RT	germination and a related SPIB cDNA is found in needles.";			
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF548021; AAN40688.1; "			
DR	GO; GO:0003793; F:defense/immunity protein activity; IEA.			
DR	InterPro; IPR008176; Gamma-thionin.			
DR	RefSeq; IPRO03614; Kncotl.			
DR	Pfam; PF00304; Gamma-thionin; 1.			
DR	ProDom; PD002594; G_Purothionin; 1.			
DR	SMART; SM00505; Kncotl; 1.			
DR	PROSITE; PS00940; GAMMA_THIONIN; 1.			
SC	SEQUENCE 83 AA; 8888 MW; E45BF9B61B9AA3D2 CRC64;			

Alignment Scores:

Pred. No.:	5,14e-05	Length:	83
Score:	118.00	Matches:	26
Percent Similarity:	51.32%	Conservative:	13
Best Local Similarity:	34.21%	Mismatches:	35
Query Match:	15.69%	Indels:	2
DB:	10	Gaps:	2

US-10-006-252A-19 (1-414) x Q8GTL2 (1-83)

QY	31	TCCATCATCGCACCTTTTTTGTCTGCTCTTTTCTTTTCTTTTCTGCTGCTTTTTCGAAGCACCACA	90	
Db	8	SerArgLeuSerAlaLeuPheLeuValLeuValIleSerIleGlyMetMetGln	27	
QY	91	ATGTTGGGAAGCAGC---	AAGTTGCGAAGGCCAAGTCGGACATGGTCAGAGTCCT	147
Db	28	LeuGluProAlaGluGlyArgThrCysLysThrProSerGlyLysPheLysGlyValCys	47	

QY	148	GGAAACAATAACGCATGCAAGAATACAGTGCATTAACTCTGAGAAAAGCAACACATGATCT	201
Db	48	AlaSerArgAsnSerCysIysAsnValCys---GlnThrGluGlyPheProSerGlySer	66
QY	208	TGCAACTATGCTTCTCCAGCTCACAAAGTGTAATGCTACTTTCCTTGT	255
Db	67	CysAspPheHisValAlaAsnArgIysCysTyrCysSerIysProCys	82
RESULT 12			
Q8GTMO		PRELIMINARY;	PRT; 105 AA.
ID	AC	Q8GTMO;	
DT	01-MAR-2003	(TREMBLrel. 23, Created)	
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE		Flower-specific defensin precursor.	
DE		NADI.	
GN		Nicotiana alata (Winged tobacco) (Persian tobacco).	
OS		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC		OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
OC		OC Lamiales; Solanales; Solanaceae; Nicotiana.	
OX		NCBI_TaxID=4087;	
RN	[1]		
RP		SEQUENCE FROM N.A.	
RA	Lay F.T., Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;		
RT	"The three-dimensional solution structure of Nadi, a new floral		
RT	defensin from Nicotiana alata and its application to a homology model		
RT	of the crop defense protein alfapP."		
RL	J. Mol. Biol. 0-0-0(2003)...		
DR	ENSL; ARS09566; XAN70999.1;		
DR	GO; GO:0003793; F:defense/immunity protein activity; IEA.		
DR	InterPro; IPR008176; Gamma-thionin.		
DR	InterPro; IPR003614; Knott1.		
DR	Pfam; PF00304; Gamma-thionin; 1.		
DR	ProDom; PD002594; G_Purothionin; 1.		
DR	SMART; SM00505; KnoE1. 1.		
DR	PROSITE; PS00940; GAMMA_THIONIN; 1.		
FT	CHAIN	26 72	FLOWER-SPECIFIC DEFENSIN.
SQ	SEQUENCE	105 AA; 11722 MW; DA7F41736CE56AC3	CRC64;
Alignment Scores:			
Pred. No.:	9.01e-05	Length:	105
Score:	116.00	Matches:	27
Percent Similarity:	53.68%	Conservative:	17
Best Local Similarity:	32.93%	Mismatches:	30
Query Match:	15.43%	Indels:	8
DB:	10	Gaps:	4
US-10-006-252A-19 (1-414) x Q8GTMO (1-105)			
QY	16	ATGGCTAAGTTGGCTGCATCATCGCACTCTTTTGTGCTGCTCTTGTTCTTTTGTCTGCT	75
Db	1	MetAlaArgSerLeuCysPheMetAlaPheAlaIleLeuAlaMetMetLeuPheValAla	20
QY	76	TTCGAAGCACCAACAATGTCGGAAGCAGACAGAAAGTTGTGCGAAGGCCAAGTGGGCATGG	135
Db	21	TyrGlu-----ValGlnAlaArgGlu---CysIysThrGluSerAsnThrPhe	35
QY	136	TCAGGAGTCTGTGGAAACAATAACGATGCAAGAAATCAGTGCATTAACCTTTGGAAGCA	195
Db	36	ProGlyIleCysIleThrIysProCysArgIysAlaCysIleSer---GluIysPhe	54
QY	196	CGACATGGATCTTGCACATGATGCTCTCCACGCTCACAAAGTGTAATGCTACTTTCCTTGT	255
Db	55	ThrAspGlyHisCysSerIysIleLeu-----ArgArgCysLeuCysThrLysProCys	72
QY	256	TAATTT 261	
Db	73	ValPhe 74	
RESULT 13			
Q40779		PRELIMINARY;	PRT; 83 AA.
ID	Q40779		

RA Yamada S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McKendree W.L., Doostdar H., McColm T.G., Mayer R.T.;
RT "cDNA cloning and expression of a gene (Accession No. Z97064) from
RT Citrus paradisi roots similar to bacterial YRN1 and HEA10 proteins
RT and an mRNA from Brassica oleracea that is wound and dark inducible
RT (PG897-127).";
RL Plant Physiol. 115:314-314(1997).
DR EMBL; AB005266; BAA21114.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003614; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knto1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
SQ SEQUENCE 105 AA; 11635 MW; B7C586CE8DB565DF CRC64;
Alignment Scores:
Pred. No.: 0.000156 Length: 105
Score: 114.00 Matches: 28
Percent Similarity: 51.22% Conservative: 14
Best Local Similarity: 34.15% Mismatches: 32
Query Match: 15.16% Indels: 8
DB: 10 Gaps: 4
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QY 16 ATGCTAAGTTGGCTCCATCGCAGCTTTCTTTTGTCTGCTCTTCTTTGTCTGCT 75
Db 1 MetAlaArgSerValCysPheMetAlaPheAlaLeuAlaValMetLeuPheValAla 20
QY 76 TTCGAAGCACCACAAATGTTGGAAGCAGACAGATTGTGCGAAGGCCAGTGGCATGG 135
Db 21 TyrAsp-----ValGluAla---LysAspCysLysThrGluSerAsnThrPhe 35
QY 136 TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACTTTGAGAAAGCA 195
Db 36 ProGlyIleCysIleThrLysProCysArgLysAlaCysIleLys---GluLysPhe 54
QY 196 CGCATGTGATCTTGCACACTATGCTTCCCAGCTCACACAGTGTATCTGCTACTTCTGT 255
Db 55 ThrAspGlyHisCysSerLysIleLeu-----ArgArgCysLeuCysThrLysProCys 72
QY 256 TAAATT 261
Db 73 ValPhe 74
RESULT 15.
Q8W434 PRELIMINARY; PRT; 75 AA.
ID Q8W434
AC Q8W434
DT 01-VAR-2002 (TREMELrel. 20, Created)
DT 01-VAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE PDF1.
GN PDF1.
OS Vigna radiata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=157791;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B20F5 9-3-2; TISSUE=Immature seed;
RA Ishimoto M., Kaga A.;
RT "Mungbean defensin";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020613; BAB82453.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR

AC Q40779;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative gamma-thionin protein precursor.
GN SP11.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Sharma P., Linneborg A.;
RT "Isolation and characterization of a cDNA encoding a gamma-thionin-
RT like protein from roots of Norway spruce";
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X91487; CAA62761.1; -
DR PIR; T14866; T14866.
DR HSP; P41964; LYXN.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knto1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW SIGNAL.
SQ SEQUENCE 83 AA; 8835 MW; B94207ADAB8FE4A5 CRC64;
Alignment Scores:
Pred. No.: 0.000117 Length: 83
Score: 115.00 Matches: 25
Percent Similarity: 52.63% Conservative: 15
Best Local Similarity: 32.89% Mismatches: 34
Query Match: 15.29% Indels: 2
DB: 10 Gaps: 2
US-10-006-252A-19 (1-414) x Q40779 (1-83)
QY 31 TCCATCATCGCACTCTTTTGTGCTCTTTTGTGCTCTTTTGTGCTCTTTTGTGCTCTT 90
Db 8 SerArgLeuSerAlaIlePheLeuLeuValLeuLeuValIleSerIleGlyMetMetGln 27
QY 91 ATGGTGGGAAGCACAG---AAGTTGTGCGAAGGCCAAGTGGACATGCTCAGGAGTCTGT 147
Db 28 LeuGluLeuAlaGluGlyArgThrCysLysThrProSerGlyLysPheLysGlyValCys 47
QY 148 GGAACAATAACGATGCAAGAACATCAGTCATTAACCTTGAGAAAGCAGCATGATCT 207
Db 48 AlaSerSerAsnAsnCysLysAsnValCys---GlnThrGluGlyPheProSerGlySer 66
QY 208 TCCAACTATGCTTCCAGCTCACAAGTATCTGCTACTTCTCTCTGT 255
Db 67 CysAspPheHisValAlaAsnArgLysCysThrCysSerLysProCys 82
[1]
RESULT 14
O24105 PRELIMINARY; PRT; 105 AA.
ID O24105
AC O24105
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Gamma-thionin.
GN NETHIO2.
OS Nicotiana excelsior.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=61185;
RN [1]
RP SEQUENCE FROM N.A.

DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G Purothionin; 1.
DR SMART; SM00505; Knot1; 1.

Alignment Scores:	
Pred. NC.:	0.000263
Score:	12.00
Percent Similarity:	45.33%
Best Local Similarity:	37.33%
Query Match:	14.89%
DB:	10
Length:	75
Matches:	28
Conservative:	6
Mismatches:	37
Indels:	4
Gaps:	2

US-10-006-252A-19 (1-414) x Q8W434 (1-75)

31	Qy	TCATCATCGCACTCTTTTGGTCTGCTCTTTTGGTCTGCTCTTTGAGCACCACAA	90
5	Db	SerLeuAlaGlyLeuCysPheLeuPheValLeuAlaGlnGluValMetVal	24
91	Qy	ATGTGGTGAAGCACACAAGTTGTGCGAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGA	150
25	Db	GlnThrGluAla---LysThrCysGluAsnLeuAlaAsnThrTyrrargGlyProCysPhe	43
151	Qy	AACAATAACGCATGCAGAAATACGTGCATTAACTTCGAGAAAGCAGACATGGATCTTC	210
44	Db	ThrThrGlySerCysAspHisCysIysAsnIysGluHisLeuArgSerGlyArgCys	63
211	Qy	AACTATGCTTCCGAGCTCACAAAGTGATCTGCTACTTTCCTTGT	255
64	Db	ArgAspAspPhe-----ArgCysTrpCysThrArgAsnCys	75

Search completed: May 11, 2004, 17:04:29
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 08:49:06 ; Search time 1784 Seconds
(without alignments)
10058.305 Million cell updates/sec

Title: US-10-006-252a-19

Perfect score: 414

Sequence: 1 gttttattagatcatggc.....caaaaaaaaaaaaaaaaaaaaaa 414*

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	414	100.0	414	6	A26875	A26875 R.sativus A
2	414	100.0	414	6	A39549	A39549 Sequence 37
3	414	100.0	414	6	A63404	A63404 Sequence 19
4	414	100.0	414	6	AR050153	AR050153 Sequence
5	414	100.0	414	6	ARI30272	ARI30272 Sequence
6	414	100.0	414	6	I23728	I23728 Sequence 48
7	414	100.0	414	6	AR207337	AR207337 Sequence
8	414	100.0	414	6	AR374914	AR374914 Sequence
9	394	95.2	395	8	RSU18557	U18557 Raphanus sa
10	255	61.6	449	6	E34290	E34290 Phage and p
11	254.2	61.4	288	6	A39553	A39553 Sequence 41
12	254.2	61.4	288	6	AR050161	AR050161 Sequence
13	254.2	61.4	288	6	ARI30280	ARI30280 Sequence
14	254.2	61.4	288	6	I23736	I23736 Sequence 58
15	249.8	60.3	457	8	RSU18556	U18556 Raphanus sa
16	242.4	58.6	403	6	A68645	A68645 Sequence 13
17	242.4	58.6	403	8	ATANTSPEC	X91916 A.thaliana
18	242.4	58.6	425	8	AY052236	AY052236 Arabidops
19	232.4	56.1	575	6	BD223249	BD223249 Method of
20	229	55.3	454	8	AY063779	AY063779 Arabidops
21	223	53.9	400	6	A68647	A68647 Sequence 15
22	219	52.9	285	6	AR014692	AR014692 Sequence
23	219	52.9	285	6	AR432392	AR432392 Sequence
24	215.8	52.1	285	6	AR014693	AR014693 Sequence
25	215.8	52.1	285	6	AR432393	AR432393 Sequence
26	212.2	51.2	451	8	BNUS9459	US9459 Brassica na
27	210.4	50.8	475	8	RSEFF3	X97319 R.sativus m
28	207	50.0	499	8	RSAPF4	AF528180 Brassica
29	206	49.8	363	8	AF528180	AF528180 Brassica
30	204.8	49.5	274	8	AY133787	AY133787 Arabidops
31	203.4	49.1	500	6	AR014686	AR014686 Sequence
32	203.4	49.1	500	6	AR432386	AR432386 Sequence
33	203	49.0	933	8	BOL311046	AJ311046 Brassica
34	202.6	48.9	364	8	AY383485	AY383485 Brassica
35	202.6	48.9	414	6	E31545	E31545 Antibacteri
36	202.6	48.9	414	8	AB012871	AB012871 Wasabia j
37	201	48.6	416	6	E31546	E31546 Antibacteri
38	199.8	48.3	243	6	AX412406	AX412406 Sequence
39	199.8	48.3	243	6	AX412601	AX412601 Sequence
40	199.8	48.3	243	6	AX651878	AX651878 Sequence
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42	199.8	48.3	243	8	AY060506	AY060506 Arabidops
43	198.2	47.9	243	6	BD174928	BD174928 Disease t
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45	198	47.8	579	11	BV010670	BV010670 MASC_STS1

ALIGNMENTS

RESULT 1	A26875	R.sativus AFPI gene.	414 bp	DNA	linear	PAT 30-NOV-2001
LOCUS	A26875	R.sativus AFPI gene.				
DEFINITION	A26875	R.sativus AFPI gene.				
ACCESSION	A26875	R.sativus AFPI gene.				
VERSION	A26875.1	GI:1247352				
KEYWORDS		Raphanus sativus (radish)				
SOURCE		Raphanus sativus				
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
		rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.				
REFERENCE		1. (bases 1 to 414)				
AUTHORS		Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J.,				
		Osborn, R.W. and Rees, S.B.				

TITLE BIOCIDAL PROTEINS
JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;
ICI PLC (GB)
FEATURES Location/Qualifiers
source 1..414
/organism="Raphanus sativus"
/mol_type="unassigned DNA"
/db_xref="taxon:3726"

ORIGIN

Query Match 100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTT 60
DB 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTT 60

QY 61 GTTCTTTTGTGCTTTTCGAAGCACCACCAATGGTGGAGCAGAGAAAGTTGGCGAAAGG 120
DB 61 GTTCTTTTGTGCTTTTCGAAGCACCACCAATGGTGGAGCAGAGAAAGTTGGCGAAAGG 120

QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
DB 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGATC 240
DB 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGATC 240

QY 241 TGTACTCTTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300
DB 241 TGTACTCTTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCAGTGCACATCATCCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360
DB 301 ACAAATAAGTCAGTGCACATCATCCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360

QY 361 GTTGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
DB 361 GTTGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414

RESULT 2

A39549 A39549 414 bp DNA linear PAT 05-MAR-1997
LOCUS Sequence 37 from Patent WO9416076.
DEFINITION A39549
ACCESSION A39549
VERSION A39549.1 GI:2295842
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 414)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;
ZENECA LTD (GB)
COMMENT Other publication AU 5820494 940815.

FEATURES

source 1..414
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTT 60
DB 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTT 60

QY 61 GTTCTTTTGTGCTTTTCGAAGCACCACCAATGGTGGAGCAGAGAAAGTTGGCGAAAGG 120
DB 61 GTTCTTTTGTGCTTTTCGAAGCACCACCAATGGTGGAGCAGAGAAAGTTGGCGAAAGG 120

QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
DB 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180

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DB 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGATC 240

QY 241 TGTACTCTTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300
DB 241 TGTACTCTTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCAGTGCACATCATCCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360
DB 301 ACAAATAAGTCAGTGCACATCATCCATGAGTGATTTTAAAGACATGTACCAGATATGTTAT 360

QY 361 GTTGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
DB 361 GTTGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414

RESULT 3

A63404 A63404 414 bp DNA linear PAT 12-MAR-1998
LOCUS Sequence 19 from Patent WO9721814.
DEFINITION A63404
ACCESSION A63404
VERSION A63404.1 GI:3717176
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.
TITLE ANTI-FUNGAL PROTEINS
JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;
ZENECA LTD (GB)
COMMENT Other publication AU 1105397 19970703.

FEATURES

source 1..414
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 414; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTT 60
DB 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTT 60

QY 61 GTTCTTTTGTGCTTTTCGAAGCACCACCAATGGTGGAGCAGAGAAAGTTGGCGAAAGG 120
DB 61 GTTCTTTTGTGCTTTTCGAAGCACCACCAATGGTGGAGCAGAGAAAGTTGGCGAAAGG 120

QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
DB 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGATC 240
DB 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGATC 240

QY 241 TGTACTCTTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300
DB 241 TGTACTCTTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300

QY 61 GTCTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAGACACAGAAGTTGTGCGAAAGG 120
 Db 61 GTCTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAGACACAGAAGTTGTGCGAAAGG 120
 QY 121 CCAAGTGGGACATGTCAGGAGCTGTGGAAACAATTAACCGATGCAAGATCAGTGCAATT 180
 Db 121 CCAAGTGGGACATGTCAGGAGCTGTGGAAACAATTAACCGATGCAAGATCAGTGCAATT 180
 QY 181 AACCTTTGAGAAAGCAGCATGGATCTTGGCAACTATGTTCCCGAGCTCACAAGTGTATC 240
 Db 181 AACCTTTGAGAAAGCAGCATGGATCTTGGCAACTATGTTCCCGAGCTCACAAGTGTATC 240
 QY 241 TGCCTACTTCCCTGTTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTAC 300
 Db 241 TGCCTACTTCCCTGTTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTAC 300
 QY 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
 Db 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

RESULT 7
 AR207337
 LOCUS 414 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 19 from patent US 6372888.
 ACCESSION AR207337
 VERSION AR207337.1 GI:21506219
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS De Samblanx, G. W. J., Broekaert, W. Frans., and Rees, S. Bronwen.
 TITLE Antifungal proteins
 JOURNAL Patent: US 6372888-A 19 16-APR-2002;
 FEATURES
 Location/Qualifiers
 source
 1..414
 /organism="unknown"
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 Query Match 100.0%; Score 414; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCAATCATCGCACTCTCTTTTGTGCTCTT 60
 Db 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCAATCATCGCACTCTCTTTTGTGCTCTT 60
 QY 61 GTCTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAGACACAGAAGTTGTGCGAAAGG 120
 Db 61 GTCTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAGACACAGAAGTTGTGCGAAAGG 120
 QY 121 CCAAGTGGGACATGTCAGGAGCTGTGGAAACAATTAACCGATGCAAGATCAGTGCAATT 180
 Db 121 CCAAGTGGGACATGTCAGGAGCTGTGGAAACAATTAACCGATGCAAGATCAGTGCAATT 180
 QY 181 AACCTTTGAGAAAGCAGCATGGATCTTGGCAACTATGTTCCCGAGCTCACAAGTGTATC 240
 Db 181 AACCTTTGAGAAAGCAGCATGGATCTTGGCAACTATGTTCCCGAGCTCACAAGTGTATC 240
 QY 241 TGCCTACTTCCCTGTTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTAC 300
 Db 241 TGCCTACTTCCCTGTTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTAC 300
 QY 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
 Db 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360

QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
 RESULT 8
 AR374914
 LOCUS 414 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 45 from patent US 6605698.
 ACCESSION AR374914
 VERSION AR374914.1 GI:40077932
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Van Amerongen, A., Fant, F., Borremans, F. A., De Samblanx, G. W., Sijtsma, L., Melloen, R. H., Puijk, W. C., Schaaper, W. M. M., Broekaert, W. F., van Gelder, W. M. J., and Rees, S. B.
 TITLE Antifungal peptides and composition thereof
 JOURNAL Patent: US 6605698-A 45 12-AUG-2003;
 FEATURES
 Location/Qualifiers
 source
 1..414
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 100.0%; Score 414; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCAATCATCGCACTCTCTTTTGTGCTCTT 60
 Db 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCAATCATCGCACTCTCTTTTGTGCTCTT 60
 QY 61 GTCTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAGACACAGAAGTTGTGCGAAAGG 120
 Db 61 GTCTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAGACACAGAAGTTGTGCGAAAGG 120
 QY 121 CCAAGTGGGACATGTCAGGAGCTGTGGAAACAATTAACCGATGCAAGATCAGTGCAATT 180
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 QY 181 AACCTTTGAGAAAGCAGCATGGATCTTGGCAACTATGTTCCCGAGCTCACAAGTGTATC 240
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 QY 241 TGCCTACTTCCCTGTTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTAC 300
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 QY 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
 Db 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGAATTTTAAGACATGTACCAGATATGTTAT 360
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

RESULT 9
 RSU18557
 LOCUS 395 bp mRNA linear P.N 07-JUL-1995
 DEFINITION Raphanus sativus antifungal protein 1 preprotein (Rs-AP1) mRNA,
 complete cds.
 ACCESSION U18557
 VERSION U18557.1 GI:644773
 KEYWORDS Raphanus sativus (radish)
 SOURCE Raphanus sativus
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

```

REFERENCE
AUTHORS
  Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
  Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
  Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
TITLE
  Small cysteine-rich antifungal proteins from radish: their role in
  host defense
JOURNAL
  Plant Cell 7, 568-573 (1995)
AUTHORS
  Terras,F.R.
TITLE
  Direct Submission
JOURNAL
  Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
  of Genetics, Applied Biological Sciences, W. De Croylaan 42,
  Heverlee, Belgium, B-3001
COMMENT
  On Feb 9, 1995 this sequence version replaced gi:609321.
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      /db_xref="taxon:3726"
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    15..254
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      /codon_start=1
      /evidence=experimental
      /product="antifungal protein 1 preprotein"
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      /gene="Rs-APP1"
    102..254
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      /function="antifungal, fungistatic"
      /notes="Evidence for antifungal activity: Analysis of two
        novel classes of antifungal proteins from radish (Raphanus
        sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
        Chem. 267, 15301-15309"
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      /evidence=experimental
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      /note="18 A nucleotides"
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    Query Match          95.2%; Score 394; DB 8; Length 395;
    Best Local Similarity 100.0%; Pred. No. 2.8e-63;
    Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY  3 TTTATTAGTCATCGCTAAGTTTGGCTCCATCGACCTCTTTTGGTGTCTTGT 62
  DB  2 TTTATTAGTCATCGCTAAGTTTGGCTCCATCGACCTCTTTTGGTGTCTTGT 61
  QY  63 TCTTTTGTGCTTTTCCGAGCCAAACAATGGTGAAGCACAGAGATTGTGCGAAGGCC 122
  DB  62 TCTTTTGTGCTTTTCCGAGCCAAACAATGGTGAAGCACAGAGATTGTGCGAAGGCC 121
  QY  123 AAGTGGACATGTCTAGGAGTCTGTGGAACAATAACGATCAAGATCAGTCAATTA 182
  DB  122 AAGTGGACATGTCTAGGAGTCTGTGGAACAATAACGATCAAGATCAGTCAATTA 181
  QY  183 CCTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCAGCTCAAGATGTATCTG 242
  DB  182 CCTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCAGCTCAAGATGTATCTG 241
  QY  243 CTACTTCCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTAC 302
  DB  242 CTACTTCCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTAC 301

303 AATAAAGTCAGTGTCTATCCATGAGTGAATTTAAGACATGTACGAGATATGTTATGT 362
DB   302 AATAAAGTCAGTGTCTATCCATGAGTGAATTTAAGACATGTACGAGATATGTTATGT 361
QY   363 TGGTTCGGTTATACAAATAAAGTTTATTATCACCA 396
DB   362 TGGTTCGGTTATACAAATAAAGTTTATTATCACCA 395

E34290      449 bp      DNA      linear      PAT 31-JAN-2002
Phage and plasmid constructed by ligating antibacterial protein
gene DNA with vector DNA, transformant microorganism and
transformant plant containing the same and antibacterial protein.
E34290      GI:18624295
KEYWORDS    JP 2000116379-A/1.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 449)
AUTHORS     Shoji,K.
TITLE       Phage and plasmid constructed by ligating antibacterial protein
            gene DNA with vector DNA, transformant microorganism and
            transformant plant containing the same and antibacterial protein
JOURNAL     Patent: JP 2000116379-A 1 25-APR-2000;
            TOYAMA PREF
COMMENT     OS Raphanus sativus L.
            PN JP 2000116379-A/1
            PD 25-APR-2000
            PF 09-OCT-1998 JP 1998288472
            PR KAZUAKI SHOJI
            PI C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10// PC
            (C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), PC
            C12N15/00,
            PC C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91) CC
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  QY  4 TTATTAGTCATCATGCTAAGTTTGGCTCCATCATCGACCTCTTTTGGTGTCTTGT 63
  DB  29 TTATTAGTCATCATGCTAAGTTTGGCTCCATCATGTCTTCTTCGCTGCTTGTGC 88
  QY  64 CTTTGTGCTGCTTTCCGAGCCAAACAATGGTGAAGCACAGAGATTGTGCGAAGGCCA 123
  DB  89 GTTGTTCGCTTTCCGAGCCAAACAATGGTGAAGCACAGAGATTGTGCGAGGCCA 148
  QY  124 AGTGGACATGTCTAGGAGTCTGTGGAACAATAACGATCAAGATCAGTCAATTAAC 183
  DB  149 AGTGGACATGTCTAGGAGTCTGTGGAACAATAACGATCAAGATCAGTCAATTAAC 208
  QY  184 CTTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCAGCTCAAGATGTATCTGC 243
  DB  209 CTTTGAGAAAGCAGCATGGGCTTGTGCAACTATGTCTTCCAGCTCAAGATGTATCTGT 268
  QY  244 TACTTTCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTT--TTATGTAATTAC 300
  DB  269 TATTTCCCTTGTAAATTCATAACTCTTTCGGTGGTTAATAGTGTGGCAATTTACATAT 328

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QY	301	ACAAATAAGTCAGTCGACATATCCATGAGTATTTTAAAGACATGTACAGATATG-TTA	359
Db	329	AATTAATAAGTTTGTGTCACATTAATTTATTAGTACCTTTATGACATGTCCAGCATATGTTTA	388
QY	360	TGTTGGTTTCGGTTATACAAATAAAAGTTTATTACACAAAAAATAAAAAA 410	
Db	389	TGTTGGTTTGGTTGTATATATAAAAAAGTTTACGGATATAATAGATGATAA 439	
RESULT 11			
LOCUS	A39553	288 bp	DNA linear PAT 05-MAR-1999
DEFINITION	Sequence 41 from Patent WO9416076.		
ACCESSION	A39553		
VERSION	A39553.1	GI:2295844	
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 288)		
AUTHORS	Dubock,A.C., Powell,K.A. and Rees,S.B.		
TITLE	ANTI-MICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS		
JOURNAL	Patent: WO 9416076-A 41 21-JUL-1994;		
COMMENT	ZENECA LTD (GB)		
FEATURES	Other publication AU 5820494 940815.		
source	1.288		
ORIGIN	Location/Qualifiers		
Query Match	61.4%; Score 254.2; DB 6; Length 288;		
Best Local Similarity	98.8%; Pred. No. 4.9e-50;		
Matches	256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	1	GTTTATTAGTATCATCGCTAAGTTTTCGGTCCATCATCGCATTTCTTTTGTGCTCTT	60
Db	28	GTTTATTAGTATCATCGCTAAGTTTTCGGTCCATCATCGCATTTCTTTTGTGCTCTT	87
QY	61	GTTCTTTTGTCTTTCGAGACCAACCAATGTTGGAACACAGAAAGTTGCCGAAAGG	120
Db	89	GTTCTTTTGTCTTTCGAGACCAACCAATGTTGGAACACAGAAAGTTGCCGAAAGG	147
QY	121	CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT	180
Db	148	CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAGTGCATT	207
QY	181	ACCTTGAGAAAGACGACATGATCTTTGCAACTATGCTTTCCAGCTCACAGTGTATC	240
Db	208	AGACTTGAGAAAGACGACATGATCTTTGCAACTATGCTTTCCAGCTCACAGTGTATC	267
QY	241	TGCTACTTTTCTTGTTAAT 259	
Db	268	TGCTACTTTTCTTGTTAAT 286	
RESULT 12			
LOCUS	AR050161	288 bp	DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 58 from patent US 5824869.		
ACCESSION	AR050161		
VERSION	AR050161.1	GI:5972153	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 288)		
AUTHORS	Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,		
TITLE	Terras,F.R.G. and Vanderleyden,J.		
JOURNAL	Biocidal proteins		
FEATURES	Patent: US 5824869-A 58 20-OCT-1998;		
	Location/Qualifiers		

of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
Location/Qualifiers
1. .457
/organism="Raphanus sativus"
/mol_type="mRNA"
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/db_xref="taxon:3726"
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1. .457
/gene="Rs-APP2"
42. .284
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/function="antifungal, fungistatic"
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/evidence=experimental
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/protein_id="AA069540.1"
/db_xref="GI:609320"
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42. .128
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129. .281
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/function="antifungal, fungistatic"
/note="Evidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"
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FEATURES
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1. .457
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novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"
/citation=[1]
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ORIGIN

Query Match 60.3%; Score 249.8; DB 8; Length 457;
Best Local Similarity 80.4%; Pred. No. 5.1e-49;
Matches 329; Conservative 0; Mismatches 76; Indels 4; Gaps 3;

QY 4 TTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTTTTGTGCTCTGTGTT 63
DB 30 TTAGTAGTATCATCGCTAAGTTTGGCTTCTATCATTTGCTCTCTCTCTCTCTCTCTGTC 89
QY 64 CTTTTTGTCTCTTTCGAAAGCACCACCAATGCTGGAAGCACAGAAAGTTGTGCGAAAGCCCA 123
DB 90 GTTTTTGTCTCTTTCGAAAGCACCACCAATGCTGGAAGCACAGAAAGTTGTGCGAGGCCA 149
QY 124 AGTGGGACATGCTCAGGAGTCTGTGGAACAAATACCGATCGACGATCAGTGCAATTAAC 183
DB 150 AGTGGGACATGCTCAGGAGTCTGTGGAACAAATACCGATCGACGATCAGTGCAATTCGA 209
QY 184 CTTGAGAAAGCACGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGTC 243
DB 210 CTTGAGAAAGCACGACATGGGCTCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGT 269
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DB 270 TATTTCCCTTGTTAATTTCCTAAATACTCTTCGGTGGTTAATAGTGTGGCATATTACATAT 329
QY 301 ACAAAATAAGTCAGTGTCACATCATCATGAGTGATTTTAAAGACATGTACCAAGATATG-TTA 359
DB 330 AATTAAATAGTTTGTGTCATTTATTATGAGTCTTTATGACATGTGCCAGGTATGTTTA 389
QY 360 TCTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAA 408
DB 390 TCTTGGTTCGGTTGTTAATAATAAAAAAGTTTACGGATAATAGATGATAA 438

Search completed: May 13, 2004, 10:11:02
Job time : 1790 secs

268 TGCTACTTTCCTTGTTAAT 286

RESULT 14
123736
LOCUS
DEFINITION
Sequence 58 from patent US 5538525.
123736
ACCESSION
VERSION
123736.1 GI:1603606
KEYWORDS
Unknown.
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 286)
Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
TITLE
Biocidal proteins
JOURNAL
Patent: US 5538525-A 58 23-JUL-1996;
FEATURES
Location/Qualifiers
1. .286
/organism="unknown"
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ORIGIN

Query Match 61.4%; Score 254.2; DB 6; Length 286;
Best Local Similarity 98.8%; Pred. No. 4.9e-50;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATCATGCTAAGTTTGGTCCATCATCGCACTCTCTTTTGTGCTCTTT 60
DB 28 GTTTTATTAGTATCATGCTAAGTTTGGTCCATCATCGCACTCTCTTTTGTGCTCTTT 87
QY 61 GTTCTTTTGTGCTTTCGAAGCACCACCAATGTTGGAAGCACAGATGTTGCGAAGG 120
DB 88 GTTCTTTTGTGCTTTCGAAGCACCACCAATGTTGGAAGCACAGATGTTGCGAAGG 147
QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGATGCAAGATCAGTGCAATT 180
DB 148 CCAAGTGGGACATGTCAGGAGTCTGTGGAACAATAACGATGCAAGATCAGTGCAATT 207
QY 181 AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATC 240
DB 208 AGACTTGGAAAGCACGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGATC 267
QY 241 TGCTACTTTCCTTGTTAAT 259
DB 268 TGCTACTTTCCTTGTTAAT 286

RESULT 15
RSU18556
LOCUS
DEFINITION
Raphanus sativus antifungal protein 2 preprotein (Rs-APP2) mRNA,
complete cds.
UI18556
ACCESSION
VERSION
UI18556.1 GI:609319
KEYWORDS
SOURCE
ORGANISM
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eucots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (sites)
Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F.,
Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
TITLE
Small cysteine-rich antifungal proteins from radish: their role in
host defense
JOURNAL
Plant Cell 7, 568-573 (1995)
REFERENCE
2 (bases 1 to 457)
Terras, F.R.
Direct Submission
TITLE
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory

CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence is given here.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.8e-92;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTTATTAGTCATCGCTAAGTTTGGCTGCATCATCGCACTTCTTTTGTGCTCTT 60
   |||||
QY 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGCGAAAGG 120
   |||||
DB 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGCGAAAGG 120
   |||||
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DB 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
   |||||
QY 181 AACCTTGAGAAAGCAGCATGATCTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
   |||||
DB 181 AACCTTGAGAAAGCAGCATGATCTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
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QY 301 ACAAAATAAGTCAGTGCATCTCCATCCATGAGTATTTAAGACATGTACCAGATATGTTAT 360
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DB 301 ACAAAATAAGTCAGTGCATCTCCATCCATGAGTATTTAAGACATGTACCAGATATGTTAT 360
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QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAA 414
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DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAA 414
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RESULT 2

AAQ70128 standard; cDNA; 414 BP.

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AC AAQ70128;
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XX 25-MAR-2003 (revised)
XX 14-FEB-1995 (first entry)
XX
XX Antimicrobial Rs-AFP1.
XX Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance;
XX Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX
XX Raphanus sativus.
XX
XX WO9416076-A1.
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB000012.
XX
XX

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PR 08-JAN-1993; 93GB-00000281.

XX (ZENE) ZENECA LTD.

XX Dubock AC, Powell KA, Rees SB;

XX WPI; 1994-249223/30.

XX P-PSDB; AAR57325.

XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.

XX Disclosure; Page 31; 39pp; English.

XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-AFP1 from *R. sativus*. The full-length cDNA
 CC sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to
 CC correct PN field.)

SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.8e-92;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTTTATTAGTCATCGCTAAGTTTGGCTGCATCATCGCACTTCTTTTGTGCTCTT 60
   |||||
DB 1 GTTTATTAGTCATCGCTAAGTTTGGCTGCATCATCGCACTTCTTTTGTGCTCTT 60
   |||||
QY 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGCGAAAGG 120
   |||||
DB 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAGCACAGAGTTGTGCGAAAGG 120
   |||||
QY 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
   |||||
DB 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
   |||||
QY 181 AACCTTGAGAAAGCAGCATGATCTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
   |||||
DB 181 AACCTTGAGAAAGCAGCATGATCTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
   |||||
QY 241 TGTACTTTCTCTTGTAAATTTATCGAAACTCTTTTGTGAATAGTTTATGTAATTTAC 300
   |||||
DB 241 TGTACTTTCTCTTGTAAATTTATCGAAACTCTTTTGTGAATAGTTTATGTAATTTAC 300
   |||||
QY 301 ACAAAATAAGTCAGTGCATCTCCATCCATGAGTATTTAAGACATGTACCAGATATGTTAT 360
   |||||
DB 301 ACAAAATAAGTCAGTGCATCTCCATCCATGAGTATTTAAGACATGTACCAGATATGTTAT 360
   |||||
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAA 414
   |||||
DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTACCAAAAAA 414
   |||||

```

RESULT 3

AAQ72333

ID AAQ72333 standard; cDNA; 414 BP.

XX AAQ72333;

XX

XX 25-MAR-2003 (revised)

XX 19-JAN-1998 (first entry)

XX Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.

XX Antifungal protein; candida; fungal resistance; food additive; radish;
 KW crop protection; plant defensin; bacterium; preservation; ss.
 XX
 XX Raphanus sativus.

```

FH Key Location/Qualifiers
FT CDS 16..258
FT /tag= a
FT sig_peptide 16..102
FT /tag= b
FT mat_peptide 103..255
FT /tag= c
FT /product= "antifungal_protein_1"
XX WO9721815-A2.
XX
XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Meloen RH, Puijk WC, Schaaper WMM, Sijtsma L, Van Amerongen A;
XX Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX Van Gelder WWJ;
XX
XX WPI; 1997-332786/30.
XX P-PSDB; AAW19280.
XX
XX Antifungal peptide derived from radish antifungal protein 2 - and related
XX DNA, useful for producing plants with increased fungal resistance and as
XX therapeutic or preservative agent.
XX
XX Claim 8; Fig 2; 65pp; English.
XX
XX This cDNA sequence encodes an Rhanus sativus (radish) antifungal
XX protein (Rs-APF1). Analogues of the homologous protein, Rs-APP2
XX (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,
XX AAW19301-04, AAW19330-34 and AAW31765-834). Plants containing DNA
XX sequences encoding these proteins have improved resistance to fungi.
XX Compositions containing the peptides can be used to control fungi or
XX bacteria in pharmaceutical (e.g. treatment of Candida infections) or
XX preservative purposes (as food additives). In agriculture, the peptide
XX may be used to improve disease resistance or disease tolerance of crops,
XX either pre or post harvest. When applied to plants they may also have
XX curative as well as protective actions. The peptides may also be used to
XX protect plants by introducing them, or a microorganism capable of
XX expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
XX PI field.)
XX
XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 414; DB 2; Length 414;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-92;
XX Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTTATTAGTATGCTAGTGGTGGTCCATCATCGCACTCTTTGCTGCTTT 60
XX DB 1 GTTTATTAGTATGCTAGTGGTGGTCCATCATCGCACTCTTTGCTGCTTT 60
XX
XX QY 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
XX DB 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
XX
XX QY 121 CCAAGTGGGACATGTCAGAGTCTGTGGAACATACGATGCAAGTCAAGTCAATT 180
XX DB 121 CCAAGTGGGACATGTCAGAGTCTGTGGAACATACGATGCAAGTCAAGTCAATT 180
XX
XX QY 181 AACCTTGAGAAACACGACATGATCTTGCACACTATGCTCCAGCTCACAAGTGTATC 240
XX DB 181 AACCTTGAGAAACACGACATGATCTTGCACACTATGCTCCAGCTCACAAGTGTATC 240
XX
XX QY 241 TGCTACTTCCCTGTTAAATTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
XX DB 241 TGCTACTTCCCTGTTAAATTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300

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Db 241 TGCTACTTCCCTGTTAAATTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
QY 301 ACAAAATAAGTCACTGCTCACTATCCATGAGTCAATTTTAAGACATGTCACAGATATGTTAT 360
Db 301 ACAAAATAAGTCACTGCTCACTATCCATGAGTCAATTTTAAGACATGTCACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414

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RESULT 4

```

AAT68696
ID AAT68696 standard; cDNA; 414 BP.
XX
XX AAT68696;
XX
XX 13-DEC-1997 (first entry)
XX
XX Radish antifungal protein 1 (Rs-APF1) cDNA.
XX
XX Rs-APF1; radish antifungal protein 1; fungicide; salt tolerance;
XX preservative; transgenic plant; crop protection.
XX
XX Raphanus sativus.
XX
XX Key Location/Qualifiers
XX CDS 16..258
XX /tag= a
XX /transl_except= (pos:85..87, aa:Glu)
XX sig_peptide 16..102
XX /tag= b
XX mat_peptide 103..255
XX /tag= c
XX
XX WO9721814-A1.
XX
XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003065.
XX
XX 13-DEC-1995; 95GB-00025474.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Broekaert WF, De Samblanx GW, Rees SB;
XX WPI; 1997-332785/30.
XX P-PSDB; AAW19617.
XX
XX New active mutants of radish antifungal protein 2 - used to generate
XX fungus-resistant plants or as therapeutic or preservative agents.
XX
XX Disclosure; Fig 2; 39pp; English.
XX
XX This cDNA clone codes for the preprotein for radish antifungal protein 1
XX (Rs-APF1) (AAW19617). Novel antifungal proteins are based on Rs-APF1, Rs-
XX APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9
XX is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by
XX Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The
XX mutants show improved salt tolerant antifungal activity, particularly
XX when expressed in plants
XX
XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 414; DB 2; Length 414;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-92;
XX Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTTATTAGTATGCTAGTGGTGGTCCATCATCGCACTCTTTGCTGCTTT 60
XX DB 1 GTTTATTAGTATGCTAGTGGTGGTCCATCATCGCACTCTTTGCTGCTTT 60

```


DR P-PSDB; ADC51224.
 XX Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.
 XX Claim 3; SEQ ID NO 3; 34pp; Japanese.
 XX The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defense) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present DNA sequence encodes a
 CC Brassica defensin protein of the invention.
 XX Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
 SQ Query Match 74.3%; Score 307.8; DB 9; Length 426;
 Best Local Similarity 88.8%; Pred. No. 4.9e-66;
 Matches 356; Conservative 0; Mismatches 42; Indels 3; Gaps 2;
 QY 16 ATGCTAAGTTTGGTCCATCAGCATTCTTTTGGCTGCTCTTTTGGCTGCT 75
 Db 1 ATGCTAAGTTTGGTCTATCATTTGCCCACTTTTGGCTGCTCTTTTGGCTGCT 60
 QY 76 TTCGAAGCACCACAAATGTTGGAGACACAGATTTGGGAGGCGCAAGTGGGACATGG 135
 Db 61 TTCGAGCACCACAAATGTTGGAGACACAGATTTGGGAGGCGCAAGTGGGACATGG 120
 QY 136 TCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 121 TCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 180
 QY 196 CGCATGATCTTGCACATATCTTCCAGCTCACAAGTATCTGCTACTTCTTCTTGT 255
 Db 181 CGCATGATCTTGCACATATCTTCCAGCTCACAAGTATCTGCTACTTCTTCTTGT 240
 QY 256 TAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTACACAAAATAAGTCAGT 315
 Db 241 TAATTTATCGCAAACTCTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
 QY 316 GTCATATCCATGAGTGATTTTAAAGACATGTACC--AGATATGTTATGTTGGTTCGGTTA 373
 Db 301 GTCATATCAATGAGTGATTTTATGACATGTACCTGATATATGTTATGTTGGTTCGGTTA 360
 QY 374 TACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
 Db 361 TA-ATAAAGTTTATGCAACCTTCAAAAAAATAAAAAA 400

RESULT 7
 AAA53190
 ID AAA53190 standard; DNA; 449 BP.
 XX AC AAA53190;
 XX 06-OCT-2000 (first entry)
 DT DT
 DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
 KW pathogenic microbe; radish; rice blast disease; ds.
 XX Raphanus sativus.
 OS JP2000116379-A.
 FN 25-APR-2000.
 PD 09-OCT-1998; 98JP-00288472.
 XX PF

XX 09-OCT-1998; 98JP-00288472.
 XX (TOYA-) TOYAMA KEN.
 XX WPI; 2000-389821/34.
 DR P-PSDB; AAY91117.
 XX Isolated DNA from Raphanus sativus used to transform a microbe and a
 PT plant to produce an antibacterial protein used to increase resistance of
 PT rice paddy against pathogenic microbes.
 XX Claim 1; Page 4; 7pp; Japanese.
 XX The present sequence encodes an antibacterial protein, designated
 CC radishin, isolated from Raphanus sativus (radish). A phage or plasmid
 CC comprising radishin can be used for increasing resistance of paddy and
 CC rice blast disease against pathogenic microbes
 XX Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
 SQ Query Match 61.6%; Score 255; DB 3; Length 449;
 Best Local Similarity 81.0%; Pred. No. 4.7e-53;
 Matches 333; Conservative 0; Mismatches 74; Indels 4; Gaps 3;
 QY 4 TTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTTGT 63
 Db 29 TTATTAGTATGATGCTAAGTTTGGTCCATCATGCTCTTCTTCTTGGCTGCTCTTGT 88
 QY 64 CTTTTTGGCTCTTTCGAAGCACCAACAATGGTGGAGCACAGAAAGTTTGGCGAAGGCCA 123
 Db 89 GTTTTTCTCTTTCGAAGCACCAACAATGGTGGAGCACAGAAAGTTTGGCGAAGGCCA 148
 QY 124 AGTGGGACATGGTCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATTAAC 183
 Db 149 AGTGGGACATGGTCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATTAAC 208
 QY 184 CTTGAGAAAGCAGACATGATGCTTCCAACTATGCTTCCAGCTCACAAGTGTATCTGTC 243
 Db 209 CTTGAGAAAGCAGACATGCTTCCAACTATGCTTCCAGCTCACAAGTGTATCTGTC 268
 QY 244 TACTTCTCTTGTATTT-TATCGCAAACTCTTGGTGAATAGTTT-TTATGTAATTTAC 300
 Db 269 TATTCCCTTGTATTTCCATAAACTCTTCGGTGGTTAATAGTGTGCGCATTTTACATAT 328
 QY 301 ACAAAATAAGTCAGTGTACTATCCATGATGATTTTAAAGACATGTACCAGATATG-TTA 359
 Db 329 AATTAATAGTTTGTCTACTATTTTATGACACTTTATGACATGTGCGAGGTATGTTTA 388
 QY 360 TGTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 410
 Db 389 TGTGGTTCGGTTATATATAAAAAAGTTTACGGATATAATAAGATGATAA 439

RESULT 8
 AAQ38652
 ID AAQ38652 standard; DNA; 261 BP.
 XX AC AAQ38652;
 XX 25-MAR-2003 (revised)
 DT 07-JUL-1993 (first entry)
 DE RS-AFP2 cDNA.
 XX Raphanus sativus; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 KW fungicide; bacteriocide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX Raphanus sativus.
 OS
 XX Key Location/Qualifiers
 FH 16..256
 FT CDS

/*tag= a

PT WO9305153-A1.
 PN 18-MAR-1993.
 PD 27-AUG-1992; 92WO-GB001570.
 PP 29-AUG-1991; 91GB-00018523.
 PR 13-FEB-1992; 92GB-00003038.
 PR 25-JUN-1992; 92GB-00013526.
 XX (ICIL) IMPERIAL CHEM IND PLC.
 PA Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 PN WPI; 1993-100978/12.
 DR Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX Example 21; Fig 35; 110pp; English.
 PS This cDNA represents the sequence of Rs-APP2 from *Raphanus sativus*. PCR
 CC primer AQ38640 was used together with AQ38641 to generate a probe for
 CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AQ38642 and AQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dUTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence was identified
 CC as Rs-APP1 (AQ38650). Rs-APP2 was seen to differ by only 2 amino acids
 CC from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
 CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Query Match 61.4%; Score 254.2; DB 2; Length 261;
 Best Local Similarity 98.8%; Pred. No. 6.5e-53;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 60
 DB 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 60
 QY 61 GTTCTTTTGTGCTTTTGGAGGACCAACAAATGGTGGAGGACAGAGAGTTGTGCGAAGG 120
 DB 61 GTTCTTTTGTGCTTTTGGAGGACCAACAAATGGTGGAGGACAGAGAGTTGTGCGAAGG 120
 QY 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
 DB 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
 QY 181 AACCTTGAGAAAGCAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGTATC 240
 DB 181 AGACTTTGAGAAAGCAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGTATC 240
 QY 241 TGCTACTTTCTCTGTTAAT 259
 DB 241 TGCTACTTTCTCTGTTAAT 259

RESULT 9
 AAQ70130
 ID AAQ70130 standard; cDNA; 288 BP.
 XX AAQ70130;
 AC AAQ70130;
 XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 DE Antimicrobial Rs-APP2.
 XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
 KW Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis; ss.
 XX *Raphanus sativus*.
 OS WO9416076-A1.
 PN 21-JUL-1994.
 PD 05-JAN-1994; 94WO-GB000012.
 PF 08-JAN-1993; 93GB-00000281.
 XX (ZENE) ZENECA LTD.
 PA Dubock AC, Powell KA, Rees SB;
 PI WPI; 1994-249223/30.
 DR P-PSDB; AAR57327.
 XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 XX Disclosure; Page 33; 39pp; English.
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APP1 from *R. sativus*. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Query Match 61.4%; Score 254.2; DB 2; Length 288;
 Best Local Similarity 98.8%; Pred. No. 6.6e-53;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 60
 DB 28 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 87
 QY 61 GTTCTTTTGTGCTTTTGGAGGACCAACAAATGGTGGAGGACAGAGAGTTGTGCGAAGG 120
 DB 88 GTTCTTTTGTGCTTTTGGAGGACCAACAAATGGTGGAGGACAGAGAGTTGTGCGAAGG 147
 QY 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 180
 DB 148 CCAAGTGGGACATGCTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT 207
 QY 181 AACCTTGAGAAAGCAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGTATC 240
 DB 208 AGACTTTGAGAAAGCAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGTATC 267
 QY 241 TGCTACTTTCTCTGTTAAT 259
 DB 268 TGCTACTTTCTCTGTTAAT 286

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RESULT 10
AAV10632
ID AAV10632 standard; DNA; 403 BP.
XX
AC AAV10632;
XX
DT 23-JUN-1998 (first entry)
XX
DE A. thaliana PDF1.1 DNA.
XX
KW Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 26..288
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
FT /product= "PDF1.1"
FT /note= "plant defensin"
XX
FN WO9800023-A2.
XX
PD 08-JAN-1998.
XX
PF 20-JUN-1997; 97WO-GB001672.
XX
PR 01-JUL-1996; 96GB-00013753.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
XX
DR WPI; 1998-086663/08.
DR P-PSDB; AAW40345.
XX
PT Protecting plants against pathogens by inducing defensin genes - by
PT stimulating ethylene or jasmonate pathways, also new promoter of defensin
PT gene from Arabidopsis.
XX
PS Disclosure; Fig 1; 72pp; English.
XX
CC This sequence encodes the Arabidopsis PDF1.1 gene which is used in a
CC novel method for the protection of plants against pathogens which
CC involves inducing expression of a plant defensin gene by stimulating the
CC jasmonate and/or ethylene pathways. The method is used to induce
CC protection against necrotrophic pathogens, specifically fungi and does
CC not require cytotoxic or potentially harmful chemicals
XX
SQ Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
Query Match 58.6%; Score 242.4; DB 2; Length 403;
Best Local Similarity 76.5%; Pred. No. 5.7e-50;
Matches 297; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATGATGGCTAAGTTTGGTCCATCATCGCATCTTTTCTGCTCTT 60
DB 11 GTTAAACAATAGTCATGGCTAAGTCTGTACATCGTTACTTTCTTCGCTGCTCT 70
QY 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGGTGGACACAGAAAGTTGCGAAAG 120
DB 71 GTTTTCTTTGCTCTTGAAGCACCAGATGGTGGTGAACACAGAAAGTTGCGAGAG 130
QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAAATACGCATGCAAGATCGTGCATT 180
DB 131 CCAAGTGGGACATGGTCGGAGTTTGGGAAACAGTAACCGTGCAGAAATCAGTGCATT 190
QY 181 AACCTTGAGAAACACGACATGGATCTTGCAACTATGCTTCCAGTCAACAAGTGTATC 240
DB 191 AACCTTGAGAAACACGACATGGATCTTGCAACTATGCTTCCAGTCAACAAGTGTATC 250
QY 241 TGCTACTTCTCTGTTTAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300
DB 251 TGCTACTTCCCATGTTAATCTACCAAGAGCTCTTAATGCTTAATATAAGTGTGTATTT 310
QY 301 ACAAATAAGTCAGTGTCACTATCCATGAGTGTATTAAGACATGTACCAGATAGTTAT 360
DB 311 CTATTAAATAAGTATGTGTCACTATGAGAGGTCTTATGACATGTACCAGATATGTTAT 370
QY 361 GTTGGTTCGGTTATACAAATAAAGTTT 388
DB 371 GTTGTCTTGTGTTTAATGAAGTAAACTTT 398
RESULT 11
AAZ99339
ID AAZ99339 standard; DNA; 575 BP.
XX
AC AAZ99339;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker peptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
XX Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..566
FT /*tag= a
FT /product= "fusion protein of DmAMP1 and RsAPP2"
XX
PN WO200011175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
XX
PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84072.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Disclosure; Fig 34; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polyprotein is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
```


XX SQ Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;
Query Match 56.1%; Score 232.4; DB 3; Length 575;
Best Local Similarity 95.6%; Pred. No. 1.8e-47;
Matches 239; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 10 GTGATCATGCTAAGTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTGCTTTT 69
DB 318 GGGCCCATGGCTAAGTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTTT 377
QY 70 GCTGCTTTGGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGGGAAGGCCAAAGTGGG 129
DB 378 GCTGCTTTGGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGGGAAGGCCAAAGTGGT 437
QY 130 ACATGTCAGAGTCTGTGAAACATTAAGCATGCAAGATGCAATTAACCTTGAG 189
DB 438 ACATGTCAGAGTCTGTGAAACATTAAGCATGCAAGATGCAATTAACCTTGAG 497
QY 190 AAAGCAGCATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTT 249
DB 498 AAAGCAGCATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTT 557
QY 250 CTTTGTAAAT 259
DB 558 CTTTGTAAAT 567
RESULT 12
AAV10633
ID AAV10633 standard; DNA; 400 BP.
AC AAV10633;
DT 23-JUN-1998 (first entry)
DE A. thaliana PDF1.2 DNA.
KW Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 32..274
FT /*tag= a
FT sig_peptide 32..119
FT /*tag= b
FT mat_peptide 120..271
FT /*tag= C
FT /product= "PDF1.2"
FT /note= "plant defensin"
XX WO9800023-A2.
XX 08-JAN-1998.
XX 20-JUN-1997; 97WO-GB001672.
XX 01-JUL-1996; 96GB-00013753.
XX (ZENE) ZENECA LTD.
XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
XX WPI; 1998-086663/08.
XX P-PSDB; AAW40346.
XX Protecting plants against pathogens by inducing defensin genes - by
PT stimulating ethylene or jasmonate pathways, also new promoter of defensin
PT gene from Arabidopsis.
XX

PS Disclosure; Fig 1; 72pp; English.
XX This sequence encodes the Arabidopsis PDF1.2 gene which is used in a
CC novel method for the protection of plants against pathogens which
CC involves inducing expression of a plant defensin gene by stimulating the
CC jasmonate and/or ethylene pathways. The method is used to induce
CC protection against necrotrophic pathogens, specifically fungi and does
CC not require cytotoxic or potentially harmful chemicals
XX
SQ Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
Query Match 53.9%; Score 223; DB 2; Length 400;
Best Local Similarity 79.9%; Pred. No. 3.3e-45;
Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;
QY 5 TATTATGATCATGCTAAGTTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTC 64
DB 21 TATATATCATCATGCTAAGTTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTC 80
QY 65 TTTTGGCTGCTTTTGAAGCACCACCAATGGTGGAGCAGACAGAAAGTTGTGGAAAGGCCAA 124
DB 81 TCTTTGCTGCTTTTGAAGCACCACCGCAATGGTGGAGCAGACAGAAAGTTGTGGAGAGCCAA 140
QY 125 GTGGGACATGGTCAGGAGTCTGTGGAACAATAAGCATGCAAGATCAGTGCATTAAACC 184
DB 141 GTGGGACATGGTCAGGAGTCTGTGGAACAATAAGCATGCAAGATCAGTGCATTAAACC 200
QY 185 TTGAGAAAGCAGCAGATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCT 244
DB 201 TTGAGAGGCCAAACATGATCATGCAACTATGCTTCCAGCAGACACAAGTGTATCTGTT 260
QY 245 ACTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGGAATAGTTTATGTAATTACACAA 304
DB 261 AGTCCCATGTTAAATCTACCACTAATCTTTGGTGCTAAATCGTGTGTTTATACATAAA 320
QY 305 AATAAGTCAGTGTCACTATCCATGATGATTTTAAGACATGTA 347
DB 321 AATAAGTCAGTGTCACTATCCATGATGATTTTAAGACATGTA 361
RESULT 13
AAT94581
ID AAT94581 standard; DNA; 500 BP.
XX AAT94581;
XX
DT 12-MAY-1998 (first entry)
DE Composite cDNA sequence for Alyssum species antifungal polypeptide.
XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
KW phytopathogenic fungus; resistance; ss.
XX Alyssum sp.
XX
XX WO9737024-A2.
XX 09-OCT-1997.
XX 27-MAR-1997; 97WO-US005709.
XX 29-MAR-1996; 96US-00627706.
XX (MONS) MONSANTO CO.
XX Liang J, Shah D, Wu Y, Rosenberger CA;
XX WPI; 1997-503109/46.
XX Alyssum antifungal polypeptide and corresponding DNA - used in the
PT production of transgenic plants resistant to phytopathogenic fungi.
XX Example 4; Page 67; 92pp; English.
PS

XX This sequence represents the cDNA sequence encoding the antifungal
 CC polypeptide AlyAFP, from plants of the genus *Alyseum*. The sequence
 CC represents a composite of the sequences isolated by 5' and 3' RACE (Rapid
 CC Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The
 CC AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst
 CC the coding DNA can be used to produce transgenic plants that express the
 CC polypeptide making them resistant to the phytopathogenic fungi
 XX
 SQ Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
 Query Match 49.1%; Score 203.4; DB 2; Length 500;
 Best Local Similarity 72.5%; Pred. No. 2.3e-40;
 Matches 317; Conservative 0; Mismatches 91; Indels 29; Gaps 3;
 QY 6 ATTAGTATCATGGCTAAGTTGGTGCATCATCGACATTCCTTTTGGCTGCTCTGCTTCT 65
 DB 59 AGTAATAGATATGGCTAAGTGTGCTTCATCATCTCCCTTGTCTCTGCTCTGCTTCT 118
 QY 66 TTTTCTGCTTTTCCGAAGCACCACCAATGGTGGAGCACAGAGTTGTGGAAAGGCCAAG 125
 DB 119 CTTTCTGCTTTTGAAGCACCAGCAATGGTGGAGTTCACGAGTGTGGAGGTCACAG 178
 QY 126 TGGACATGTCGACAGAGTCTGTGGAACATTAACGATGCAAGATCAGTGCATTAACCT 185
 DB 179 TGGAAACATGGTCAAGCGTGTGTGGGAATAATAACGATGCAAGCAATGCGAAACCT 238
 QY 186 TGAGAAAGCAGACATGATCTTCAACTATGCTTCCAGCTCACAAGTGTATCTGCTA 245
 DB 239 TGAAGACAGACACAGGATCTTCACTAATGCTTCCAGCTCACAAGTGTATCTGCTA 298
 QY 246 CTTTCTGCTTTAATTAATTCGCAACTCTTTGGTG-----AATAGTTTTT 289
 DB 299 CTTCCCATGTTAATCTACCAATCACATTTTGTGTGTGTGTATTTTACATGTTATG 358
 QY 290 ATGTAAATTTACAAATAAGTCAGTGTCTACTATCCATGATGATTTTAAAGCATGTACC 349
 DB 359 TGTTTATTTACGAAATAGTCTGTGTGCA-TCCTTAAGGTGACCTTATGACATGTACC 417
 QY 350 AGATATGTTAT-----GTTGGTTCGGTTATACAAATAAAGTTTTTATCACCAA 397
 DB 418 AGATATATCATATGATGTGTGTTTGTGTGGCAATTATAAACTTTTATTTGTGGA 477
 QY 398 AAAAAAARAAAAA 414
 DB 478 TCGAAAAAARAAAAA 494

RESULT 14
 AAZ39123
 ID AAZ39123 standard; cDNA to mRNA; 414 BP.
 XX
 AC AAZ39123;
 XX
 DT 15-SEP-2003 (revised)
 DT 01-MAR-2000 (first entry)
 XX
 DE Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
 XX
 KW Wasabia japonica; antibacterial; food additive; ds.
 XX
 OS Eutrema wasabi.
 XX
 FH Key Location/Qualifiers
 FT 1. .243
 FT /tag= a
 FT /product= "antibacterial protein"
 XX
 JF11313678-A.
 XX
 PD 16-NOV-1999.
 XX
 PD 30-APR-1998; 98JP-00121303.
 XX
 PD 30-APR-1998; 98JP-00121303.
 XX
 PA (IWAT-) IWATE KEN.

XX 30-APR-1998; 98JP-00121303.
 XX (IWAT-) IWATE KEN.
 XX WPI; 2000-057353/05.
 DR P-PSDB; AAY57564.
 XX
 XX An antibacterial proein gene of *Wasabia japonica* - useful as a food- or
 PT feed-additive.
 XX
 PS Claim 3; Page 12-13; 16pp; Japanese.
 XX
 CC The present sequence encodes an antibacterial protein isolated from
 CC *Wasabia japonica*. The antibacterial protein can be used as a food or feed
 CC additive. (Updated on 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other;
 Query Match 48.9%; Score 202.6; DB 3; Length 414;
 Best Local Similarity 88.4%; Pred. No. 3.5e-40;
 Matches 220; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 16 ATGCTAAGTTTGGTGCATCATCGCTCTTCTTGGCTGCTCTTCTTCTTCTTCTGCT 75
 DB 1 ATGCTAAGTTTGGTGCATCATCGCTCTTCTTGGCTGCTCTTCTTCTTCTTCTTCTGCT 60
 QY 76 TTCGAGACACCAACATCGTGGAGCAGAGTGTGCGAAGCCCAAGTGGGACATGG 135
 DB 61 TTTGAGACACCAATCAATGTGGAGCGCAGAGTGTGCGAAGTCAAGTGGGACATGG 120
 QY 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 DB 121 TCAGGAGTCTGTGGAAACAACAATCGTGGAGTCAAGTGCATCAACCTTGAGGAGCA 180
 QY 196 CGCATGATCTTGCACATATGCTCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTGT 255
 DB 181 CGCATGATCTTGCACATATATCTTCCATATCATTCCATATCAGATGTATCTGTTCTTCCCATGT 240
 QY 256 TAATTTATC 264
 DB 241 TAATTTATC 249
 RESULT 15
 AAZ39124
 ID AAZ39124 standard; cDNA to mRNA; 416 BP.
 XX
 AC AAZ39124;
 XX
 DT 15-SEP-2003 (revised)
 DT 01-MAR-2000 (first entry)
 XX
 DE Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:3.
 XX
 KW Wasabia japonica; antibacterial; food additive; ds.
 XX
 OS Eutrema wasabi.
 XX
 FH Key Location/Qualifiers
 FT 1. .243
 FT /tag= a
 FT /product= "antibacterial protein"
 XX
 JF11313678-A.
 XX
 PD 16-NOV-1999.
 XX
 PD 30-APR-1998; 98JP-00121303.
 XX
 PD 30-APR-1998; 98JP-00121303.
 XX
 PA (IWAT-) IWATE KEN.

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XX WPI: 2000-057353/05.
DR P-PSDB; ANY57565.
XX
PT An antibacterial protein gene of Wasabia japonica - useful as a food- or
PT feed-additive.
XX
PS Claim 3; Page 13-14; 16pp; Japanese.
XX
CC The present sequence encodes an antibacterial protein isolated from
CC Wasabia japonica. The antibacterial protein can be used as a food or feed
CC additive. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 416 BP; 111 A; 77 C; 81 G; 147 T; 0 U; 0 Other;
Query Match 48.6%; Score 201; DB 3; Length 416;
Best Local Similarity 88.0%; Pred. No. 8.6e-40;
Matches 219; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 16 ATGGCTAAGTTTGGCTCCATCGACATGCTTTTGGCTGCTCTTCTTTTGGCTGCT 75
Db 1 ATGGCTAAGTTTGGCTTCTATCATGCTTCTTCTTCTGCTGCTTCTTCTTCTTCT 60
Qy 76 TTCGAAGCACCACCAATGTTGGAAGCACAGAGTTGTGGAAGGCCAAGTGGGACATGG 135
Db 61 TTTGAAGCACCACCAATGTTGGAAGGCCAAGTGTGGAAGTCAAGTGGGACATGG 120
Qy 136 TCAGGAGTCTGTGGAACAACAATACCGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 121 TCAGGAGTCTGTGGAACAACAATACCGCATGCAAGATCAGTGCATTAACTTGAGGAGCA 180
Qy 196 CGACATGGATCTTGCAACTATGTTCTTCCAGCTCACAAGTGTATCTGCTACTTTCTTGT 255
Db 181 CGACATGGATCTTGCAACTATGTTCTTCCATATCAGATGTATCTGCTACTTCCATGT 240
Qy 256 TAATTATC 264
Db 241 TAATTATC 249

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OM nucleic - nucleic search, using sw model

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Title: US-10-006-252A-19
Perfect score: 414
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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4: /cgn2_6/ptodata/2/ina/6B COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	414	100.0	414	1	US-08-377-687-48
2	414	100.0	414	1	US-08-377-687-48
3	414	100.0	414	3	US-08-971-982-48
4	414	100.0	414	4	US-09-077-951-19
5	414	100.0	414	4	US-09-077-948A-45
6	254.2	61.4	288	1	US-08-377-687-58
7	254.2	61.4	288	1	US-08-377-687-58
8	254.2	61.4	288	3	US-08-971-982-58
9	219	52.9	285	1	US-08-627-706-16
10	219	52.9	285	3	US-09-103-489-16
11	219	52.9	285	4	US-09-829-381D-16
12	215.8	52.1	285	1	US-08-627-706-17
13	215.8	52.1	285	3	US-09-103-489-17
14	215.8	52.1	285	4	US-09-829-381D-17
15	203.4	49.1	500	1	US-08-627-706-9
16	203.4	49.1	500	3	US-09-103-489-9
17	203.4	49.1	500	4	US-09-829-381D-9
18	194.6	47.0	308	1	US-08-627-706-5
19	194.6	47.0	308	3	US-09-103-489-5
20	194.6	47.0	308	4	US-09-829-381D-5
21	180	43.5	270	1	US-08-627-706-14
22	180	43.5	270	3	US-09-103-489-14
23	180	43.5	270	4	US-09-829-381D-14
24	178.8	43.2	286	1	US-08-627-706-12
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30	104.2	25.2	306	1	US-08-627-706-8
31	104.2	25.2	306	3	US-09-103-489-8
32	104.2	25.2	306	4	US-09-829-381D-8
33	74.6	18.0	243	4	US-09-732-210-11
34	50.8	12.3	150	1	US-08-377-687-33
35	50.8	12.3	150	1	US-08-377-687-34
36	50.8	12.3	150	1	US-08-377-192-33
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38	50.8	12.3	150	3	US-08-971-982-33
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40	50.6	12.2	565	4	US-09-589-733C-6
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44	39.6	9.6	1318	4	US-09-719-108-5
45	39.2	9.5	568	1	US-08-582-257-20

ALIGNMENTS

RESULT 1
US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BICIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48

Query Match 100.0%; Score 414; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.4e-107;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTTT 60
DB 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTTT 60
QY 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCACAAGCTTTCGGAAGG 120
DB 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCACAAGCTTTCGGAAGG 120
QY 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACCAATAACGATGCAAGATCAGTGCAATT 180
DB 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACCAATAACGATGCAAGATCAGTGCAATT 180
QY 181 AACCTTGAGAAAGCAGCATGATGCTTCCAGTATGCTTCCAGCTCACAAGTGATC 240
DB 181 AACCTTGAGAAAGCAGCATGATGCTTCCAGTATGCTTCCAGCTCACAAGTGATC 240
QY 241 TGCTACTTCTTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
DB 241 TGCTACTTCTTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
QY 301 ACAAATAAGTCACTATCCATGAGTGATTTTAAGACATGTACAGATATGTTAT 360
DB 301 ACAAATAAGTCACTATCCATGAGTGATTTTAAGACATGTACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414
DB 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414

RESULT 2

US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/POCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLSCULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; US-08-777-192-48
Query Match 100.0%; Score 414; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.4e-107;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTTT 60
DB 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTTT 60
QY 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCACAAGCTTTCGGAAGG 120
DB 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCACAAGCTTTCGGAAGG 120
QY 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACCAATAACGATGCAAGATCAGTGCAATT 180
DB 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACCAATAACGATGCAAGATCAGTGCAATT 180
QY 181 AACCTTGAGAAAGCAGCATGATGCTTCCAGTATGCTTCCAGCTCACAAGTGATC 240
DB 181 AACCTTGAGAAAGCAGCATGATGCTTCCAGTATGCTTCCAGCTCACAAGTGATC 240
QY 241 TGCTACTTCTTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
DB 241 TGCTACTTCTTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
QY 301 ACAAATAAGTCACTATCCATGAGTGATTTTAAGACATGTACAGATATGTTAT 360
DB 301 ACAAATAAGTCACTATCCATGAGTGATTTTAAGACATGTACAGATATGTTAT 360
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DB 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414

RESULT 3

US-08-971-982-48
; Sequence 48, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997

CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/002,480
 FILING DATE: 04-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 414 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 16..255
 SEQUENCE DESCRIPTION: SEQ ID NO: 48:
 US-08-971-982-48

Query Match 100.0%; Score 414; DB 3; Length 414;
 Best Local Similarity 100.0%; Pred. No. 7.4e-107;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGATCGTAAAGTTTGGTCCCATCATCGCACTCTTTTCTGCTCTT 60
 DB 1 GTTTATTAGTATGATCGTAAAGTTTGGTCCCATCATCGCACTCTTTTCTGCTCTT 60

QY 61 GTTCTTTTCTGCTTTTGAAGCACCACCAATGGTGGAAAGCAGAAAGTTGCGAAAGG 120
 DB 61 GTTCTTTTCTGCTTTTGAAGCACCACCAATGGTGGAAAGCAGAAAGTTGCGAAAGG 120

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGAAATCAGTGCATT 180
 DB 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGAAATCAGTGCATT 180

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
 DB 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240

QY 241 TGCATCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
 DB 241 TGCATCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCACTGTCACATCCATGATGATTTTAAAGCATGTACCAAGTGTAT 360
 DB 301 ACAAATAAGTCACTGTCACATCCATGATGATTTTAAAGCATGTACCAAGTGTAT 360

QY 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414
 DB 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414

RESULT 4
 US-09-077-951-19
 Sequence 19, Application US/09077951
 Patent No. 6372888
 GENERAL INFORMATION:
 APPLICANT: De Samblanx, Geneveva
 APPLICANT: Broekaert, Willem
 APPLICANT: Rees, Sarah
 TITLE OF INVENTION: Antifungal Proteins
 FILE REFERENCE: PPD50093
 CURRENT APPLICATION NUMBER: US/09/077,951
 CURRENT FILING DATE: 1999-03-11
 EARLIER APPLICATION NUMBER: GB 9525474.4
 EARLIER FILING DATE: 1995-12-13
 EARLIER APPLICATION NUMBER: PCT/GB96/03065
 EARLIER FILING DATE: 1996-12-12

NUMBER OF SEQ ID NOS: 77
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 19
 LENGTH: 414
 TYPE: DNA
 ORGANISM: Raphanus sativus
 US-09-077-951-19

Query Match 100.0%; Score 414; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 7.4e-107;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGATCGTAAAGTTTGGTCCCATCATCGCACTCTTTTCTGCTCTT 60
 DB 1 GTTTATTAGTATGATCGTAAAGTTTGGTCCCATCATCGCACTCTTTTCTGCTCTT 60

QY 61 GTTCTTTTCTGCTTTTGAAGCACCACCAATGGTGGAAAGCAGAAAGTTGCGAAAGG 120
 DB 61 GTTCTTTTCTGCTTTTGAAGCACCACCAATGGTGGAAAGCAGAAAGTTGCGAAAGG 120

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGAAATCAGTGCATT 180
 DB 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGAAATCAGTGCATT 180

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
 DB 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240

QY 241 TGCATCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
 DB 241 TGCATCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCACTGTCACATCCATGATGATTTTAAAGCATGTACCAAGTGTAT 360
 DB 301 ACAAATAAGTCACTGTCACATCCATGATGATTTTAAAGCATGTACCAAGTGTAT 360

QY 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414
 DB 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAA 414

RESULT 5
 US-09-077-948A-45
 Sequence 45, Application US/09077948A
 Patent No. 6605698
 GENERAL INFORMATION:
 APPLICANT: Van Amerongen, Aart
 APPLICANT: Fant, Franky
 APPLICANT: Borremans, Frans
 APPLICANT: De Samblanx, Geneveva
 APPLICANT: Sitjtsma, Lolke
 APPLICANT: Melloer, Robbert
 APPLICANT: Puijk, Wouter
 APPLICANT: Schaaper, Wilhelmus
 APPLICANT: Broekaert, Willem
 APPLICANT: Van Gelder, Wilhelmus
 APPLICANT: Rees, Sarah
 TITLE OF INVENTION: Antifungal Proteins
 FILE REFERENCE: 109846-257(SYN-035)
 CURRENT APPLICATION NUMBER: US/09/077,948A
 CURRENT FILING DATE: 1998-08-07
 PRIOR APPLICATION NUMBER: PCT/GB96/03068
 PRIOR FILING DATE: 1996-12-12
 PRIOR APPLICATION NUMBER: GB 9606552.9
 PRIOR FILING DATE: 1996-03-28
 PRIOR APPLICATION NUMBER: GB 9525455.3
 PRIOR FILING DATE: 1995-12-13
 NUMBER OF SEQ ID NOS: 141
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 45
 LENGTH: 414
 TYPE: DNA
 ORGANISM: Raphanus sativus

US-09-077-948A-45

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.4e-107;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTTCTTTTGGTCTCTT 60
DB 1 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTTCTTTTGGTCTCTT 60
QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 120
DB 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 120
QY 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGTGTGCGAAT 180
DB 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGTGTGCGAAT 180
QY 181 AACCTTGAGAACGACGATGATCTTTCGAACTATGCTTCCACGTCACAAGTGTATC 240
DB 181 AACCTTGAGAACGACGATGATCTTTCGAACTATGCTTCCACGTCACAAGTGTATC 240
QY 241 TGTCTACTTCTCTGTTTAACTTATCGCAAACTCTTGTGTAATAGTTTATGTAATTTAC 300
DB 241 TGTCTACTTCTCTGTTTAACTTATCGCAAACTCTTGTGTAATAGTTTATGTAATTTAC 300
QY 301 ACAAATAAGTCAGTGCATCATCATGATGATTTAAGACATGACAGATATGTTAT 360
DB 301 ACAAATAAGTCAGTGCATCATCATGATGATTTAAGACATGACAGATATGTTAT 360
QY 361 GTTGTCTGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
DB 361 GTTGTCTGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

RESULT 6

US-08-377-687-58
; Sequence 58, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 59042/SEE.36525/US/A
; TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..282
US-08-377-687-58

Query Match 61.4%; Score 254.2; DB 1; Length 288;
Best Local Similarity 98.8%; Pred. No. 3.9e-62;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTTCTTTTGGTCTCTT 60
DB 28 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTTCTTTTGGTCTCTT 87
QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 120
DB 88 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 147
QY 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGTGTGCGAAT 180
DB 148 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGTGTGCGAAT 207
QY 181 AACCTTGAGAACGACGATGATCTTTCGAACTATGCTTCCACGTCACAAGTGTATC 240
DB 208 AGACTTGAGAACGACGATGATCTTTCGAACTATGCTTCCACGTCACAAGTGTATC 267
QY 241 TGTCTACTTCTCTGTTTAACTTAT 259
DB 268 TGTCTACTTCTCTGTTTAACTTAT 286

RESULT 7

US-08-777-192-58
; Sequence 58, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43...282
 US-08-777-192-58

Query Match 61.4%; Score 254.2; DB 1; Length 288;
 Best Local Similarity 98.8%; Pred. No. 3.9e-62;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
 Db GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87
 QY 61 GTTCTTTTGTGCTTTTGGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 120
 Db GTTCTTTTGTGCTTTTGGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 147
 QY 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
 Db CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 207
 QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
 Db AGACTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 267
 QY 241 TGCTACTTTCCTTGTAAAT 259
 Db TGCTACTTTCCTTGTAAAT 286

RESULT 8
 US-08-971-982-58
 Sequence 58, Application US/08971982
 Patent No. 6187904
 GENERAL INFORMATION:
 APPLICANT: BROKERT, WILLEM F.
 CAMMUE, BRUNO P.A.
 OSBORN, RUPERT W.
 REES, SARAH B.
 TERRAS, FRANKY R.G.
 VANDERLEYDEN, JOZEF
 TITLE OF INVENTION: BIOCIDAL PROTEINS
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: CUSHMAN DAREY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 APPLICATION NUMBER: US/08/971,982
 FILING DATE: 17-NO. 6187904-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/002,480
 FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43...292
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 US-08-971-982-58

Query Match 61.4%; Score 254.2; DB 3; Length 288;
 Best Local Similarity 98.8%; Pred. No. 3.9e-62;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
 Db GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87
 QY 61 GTTCTTTTGTGCTTTTGGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 120
 Db GTTCTTTTGTGCTTTTGGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 147
 QY 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
 Db CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 207
 QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
 Db AGACTTGAGAAAGCAGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 267
 QY 241 TGCTACTTTCCTTGTAAAT 259
 Db TGCTACTTTCCTTGTAAAT 286

RESULT 9
 US-08-627-706-16
 Sequence 16, Application US/08627706
 Patent No. 5773696
 GENERAL INFORMATION:
 APPLICANT: Liang, Jihong
 APPLICANT: Shah, Dilip M.
 APPLICANT: Wu, Yonnie S.
 APPLICANT: Rosenberger, Cindy A.
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 STREET: 700 Chesterfield Village Parkway No. 5773696th
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 APPLICATION NUMBER: US/08/627,706
 FILING DATE:
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16

Query Match 52.9%; Score 219; DB 1; Length 285;
Best Local Similarity 90.3%; Pred. No. 2.8e-52;
Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GTTTATTAGTGCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTTTTGGCTGCTCTT 60
DB 16 GTTTATTAGTGCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTCTTTGCTGCTC 75
QY 61 GTTCTTTTGTGCTTTTGAAGCACCACAACTGGTGGAGGACAGAAAGTTGTGCGAAGG 120
DB 76 GTTCTTTTGTGCTTTTGAAGCACCACAACTGGTGGAGGACAGAAAGTTGTGCGAAGG 135
QY 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAACAACTAATCGCATGCAAGATCAGTGCATT 180
DB 136 CCATCAGGAGCTTGTCTCAGGAGTCTGTGGAACAACTAATCGCATGCAAGATCAGTGCATT 195
QY 181 AACCTTGAGAAAGCAGCATGGAATCTTGCACCTATGTCTTCCAGCTCACAAGTGTATC 240
DB 196 AACCTTGAGAAAGCAGCATGGAATCTTGCACCTATGTCTTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTTCCATGCTAAT 259
DB 256 TGCTACTTTTCCATGCTAAT 274

RESULT 10
US-09-103-489-16
Sequence 16, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-16

Query Match 52.9%; Score 219; DB 3; Length 285;
Best Local Similarity 90.3%; Pred. No. 2.8e-52;
Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GTTTATTAGTGCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTTTTGGCTGCTCTT 60
DB 16 GTTTATTAGTGCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTCTTTGCTGCTC 75
QY 61 GTTCTTTTGTGCTTTTGAAGCACCACAACTGGTGGAGGACAGAAAGTTGTGCGAAGG 120
DB 76 GTTCTTTTGTGCTTTTGAAGCACCACAACTGGTGGAGGACAGAAAGTTGTGCGAAGG 135
QY 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAACAACTAATCGCATGCAAGATCAGTGCATT 180
DB 136 CCATCAGGAGCTTGTCTCAGGAGTCTGTGGAACAACTAATCGCATGCAAGATCAGTGCATT 195
QY 181 AACCTTGAGAAAGCAGCATGGAATCTTGCACCTATGTCTTCCAGCTCACAAGTGTATC 240
DB 196 AACCTTGAGAAAGCAGCATGGAATCTTGCACCTATGTCTTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTTCCATGCTAAT 259
DB 256 TGCTACTTTTCCATGCTAAT 274

RESULT 11
US-09-829-381D-16
Sequence 16, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent in version 3.1
SEQ ID NO 16
LENGTH: 285
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-829-381D-16

Query Match 52.9%; Score 219; DB 4; Length 285;
Best Local Similarity 90.3%; Pred. No. 2.8e-52;
Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GTTTATTAGTGCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTTTTGGCTGCTCTT 60
DB 16 GTTTATTAGTGCATCGCTAAGTTTGGCGTCCATCATCGCACTCTCTCTTTGCTGCTC 75

QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCAGACAGAAATGTTGCGAAAGG 120
 Db GTTCTTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCAGACAGAAATGTTGCGAGG 135
 QY 121 CCAAGTGGGATGTTGAGGAGTCTGTGGAAACAAATGCGATGCAAGATGAGTGCATT 180
 Db CCATCAGGAGTCTGTGAGGAGTCTGTGGAAACAAATGCGATGCAAGATGAGTGCATT 195
 QY 181 AACCTTGAGAAAGCAGACATGATCTTGCACATGATCTTCCAGCTCACAAGTGTATC 240
 Db AACCTTGAGAAAGCAGACATGATCTTGCACATGATCTTCCAGCTCACAAGTGTATC 240
 QY 241 TGCTACTTTCTTGTAAAT 259
 Db TGCTACTTTCTTGTAAAT 274

RESULT 12
 US-08-627-706-17
 ; Sequence 17, Application US/08627706
 ; Patent No. 5773696
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yennie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 ; STREET: 700 Chesterfield Village Parkway No. 5773696th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/627,706
 ; FILING DATE:
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cohen, Charles E.
 ; REGISTRATION NUMBER: 34,565
 ; REFERENCE/DOCKET NUMBER: 38-21(10700)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314)537-6224
 ; TELEFAX: (314)537-6047
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 285 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "synthetic DNA"
 ; US-08-627-706-17

Query Match 52.1%; Score 215.8; DB 1; Length 285;
 Best Local Similarity 89.6%; Pred. No. 2.2e-51;
 Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
 Db GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 75
 QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCAGACAGAAATGTTGCGAAAGG 120
 Db GTTCTTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCAGACAGAAATGTTGCGAAAGG 135

QY 121 CCAAGTGGGATGTTGAGGAGTCTGTGGAAACAAATGCGATGCAAGATGAGTGCATT 180
 Db CCATCAGGAGTCTGTGAGGAGTCTGTGGAAACAAATGCGATGCAAGATGAGTGCATT 195
 QY 181 AACCTTGAGAAAGCAGACATGATCTTGCACATGATCTTCCAGCTCACAAGTGTATC 240
 Db AACCTTGAGAAAGCAGACATGATCTTGCACATGATCTTCCAGCTCACAAGTGTATC 240
 QY 241 TGCTACTTTCTTGTAAAT 259
 Db TGCTACTTTCTTGTAAAT 274

RESULT 13
 US-09-103-489-17
 ; Sequence 17, Application US/09103489
 ; Patent No. 6215048
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yennie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 ; STREET: 700 Chesterfield Village Parkway No. 6215048th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/103,489
 ; FILING DATE: 24-JUN-1998
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cohen, Charles E.
 ; REGISTRATION NUMBER: 34,565
 ; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 537-6224
 ; TELEFAX: (314) 537-6047
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 285 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "synthetic DNA"
 ; US-09-103-489-17

Query Match 52.1%; Score 215.8; DB 3; Length 285;
 Best Local Similarity 89.6%; Pred. No. 2.2e-51;
 Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
 Db GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 75
 QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCAGACAGAAATGTTGCGAAAGG 120
 Db GTTCTTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCAGACAGAAATGTTGCGAAAGG 135
 QY 121 CCAAGTGGGATGTTGAGGAGTCTGTGGAAACAAATGCGATGCAAGATGAGTGCATT 180

Db 136 CCATCAGGACTTGGTCAGGAGTCTGCGGAAACAAACACGATGCAAGAACCAATGCATC 195
QY 181 AACCTTGAGAAAGCAGCATGGATCTGCAACTATCTCTCCAGCTCACAAGTGTATC 240
Db 196 AGACTCGAAGAGCAGGATGATCTTGCACAACTACGCTCTCCAGCTCACAAGTGCATC 255
QY 241 TGCTACTTTCCTTGTAAAT 259
Db 256 TGCTACTTTCCTGCTAAAT 274

RESULT 14

US-09-829-381D-17
; Sequence 17, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-17

Query Match 52.1%; Score 215.8; DB 4; Length 285;
Best Local Similarity 89.6%; Pred. No. 2.2e-51;
Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGATCGCTAAGTTGGCTCCATCATCGCACTCTTTTCTGCTCTT 60
Db 16 GTTTATTAGTATGATCGCTAAGTTGGCTCCATCATCGCACTCTTTTCTGCTCTC 75
QY 61 GTTCTTTTGTCTTTTCGAGGACCAACAAATGGTGAAGCAGACAGAAAGTTGCGAAAG 120
Db 76 GTTCTTTTGTCTTTTCGAGGACCAACAAATGGTGAAGCAGACAGAAAGTTGCGAAAG 135
QY 121 CCAAGTGGGACATGCTCAGGAGTCTTGGAAACATTAACGATGCAAGATCAGTGCAT 180
Db 136 CCATCAGGAGCTTGGTCAGGAGTCTGCGGAAACAAACAGCATGCAAGAACCAATGCATC 195
QY 181 AACCTTGAGAAAGCAGCATGGATCTTGCACAACTATGCTTCCAGCTCACAAGTGTATC 240
Db 196 AGACTCGAAGAGCAGCATGGATCTTGCACAACTATGCTTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTCCTTGTAAAT 259
Db 256 TGCTACTTTCCTGCTAAAT 274

RESULT 15

US-08-627-706-9
; Sequence 9, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-627-706-9
Query Match 49.1%; Score 203.4; DB 1; Length 500;
Best Local Similarity 72.5%; Pred. No. 8.4e-48;
Matches 317; Conservative 0; Mismatches 91; Indels 29; Gaps 3;
QY 6 ATTAGTATGATCGCTAAGTTGGCTCCATCATCGCACTCTTTTGTGCTCTTGTCT 65
Db 59 AGTAATAGATATGCTAAGTGTCTTCCATCATCTCCCTGTCTCTGCTCTTGTCT 118
QY 66 TTTTCTGCTCTTCCAGCAGCAACATGTTGGAGGAGCAGCAAGTTGCGAAGGCCAAG 125
Db 119 CTTTCTGCTCTTTGAAGCAGCAGCAATGGTGGAGTCAAGAAAGTTGGAGAGTCCAAG 178
QY 126 TGGGACATGGTCAGGAGTCTGTGAAACAAATAACGATGCAAGAAATCAGTGCATTAACCT 185
Db 179 TGAACATGGTCAGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAG 238
QY 186 TGAGAAAGCAGCATGATCTTGCACAACTATGCTTCCAGCTCACAAGTGTATGCTA 245
Db 239 TGAAGAGCAGCAACGAGTCTTGCACAACTATGCTTCCAGCTCACAAGTGTATGCTA 298
QY 246 CTTTCTGCTTAAATTTATCGCAAACTCTTTGGTG-----AATAGTTTTT 289
Db 299 CTTTCCATGTTAACTACCAAACTCTTTGGTGTTGTGTGTATTTTACATGTATG 358
QY 290 AGTAATTTACACAAATAAGTGTGCTACTTCCAGCTCACAAGTGTATGCTA 349
Db 359 TGTATTATTTACATGAAATAAGTGTGCTCA-TCCCTATGGGTGACCTATGACATGTACC 417
QY 350 AGATATGTTAT-----GTTGGTTGGTTATACAAATAAAGTTTATTCACCAA 397
Db 418 AGATATATCATATATGATGTTGGTTGTTGTGGCAATTATATAACTTTTATTGTGGA 477
QY 398 AAAAAAAAAAAAAA 414
Db 478 TCAAAAAAAAAAAAAA 494

Search completed: May 13, 2004, 10:54:47
JOB time : 85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:35:52 ; Search time 336 Seconds
(without alignments)
5581.596 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 414
Sequence: 1 gttttattgatcatggc.....caaaaaaaaaaaaaaaaaa 414

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
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12: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
13: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	414	100.0	414	9	US-09-759-584-48
2	414	100.0	414	13	US-10-388-361A-45
3	414	100.0	414	14	US-10-006-252A-19
4	254.2	61.4	288	9	US-09-759-584-58
5	242.4	58.6	403	9	US-09-732-561-13
6	223	53.9	400	9	US-09-732-561-15
7	223	53.9	400	9	US-09-887-576-607
8	219	52.9	285	9	US-09-829-381A-16
9	215.8	52.1	285	13	US-10-681-972-16
10	215.8	52.1	285	13	US-09-829-381A-17
11	203.4	49.1	500	9	US-10-681-972-17
12	203.4	49.1	500	9	US-09-829-381A-9
13	203.4	49.1	500	13	US-10-681-972-9
14	196.6	47.5	243	9	US-09-938-842A-2046

ALIGNMENTS

RESULT 1
US-09-759-584-48
; Sequence 48, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSEORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 48:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 414 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 16..255
 ; US-09-759-584-48

Query Match 100.0%; Score 414; DB 9; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.3e-101;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGTCTCTT 60
 Db 1 GTTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGTCTCTT 60
 QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
 Db 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
 QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
 Db 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
 QY 181 AACCTTGAGAAAGCAGCATGGATCTTGGCAACTTGTCCAGCTCACAAGTGTATC 240
 Db 181 AACCTTGAGAAAGCAGCATGGATCTTGGCAACTTGTCCAGCTCACAAGTGTATC 240
 QY 241 TGTACTTCTCTTCTTAACTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
 Db 241 TGTACTTCTCTTCTTAACTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
 QY 301 ACAAAATAGTCAGTGCACATCCATGAGTATTTTAAAGCATGTACAGATATGTTAT 360
 Db 301 ACAAAATAGTCAGTGCACATCCATGAGTATTTTAAAGCATGTACAGATATGTTAT 360
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

RESULT 2

US-10-388-361A-45
 ; Sequence 45, Application US/10388361A
 ; Publication No. US20030226169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Amerongen, Aart
 ; APPLICANT: Pant, Franky
 ; APPLICANT: Borremans, Frans
 ; APPLICANT: De Samblanx, Genevieve
 ; APPLICANT: Sijtsma, Lolke
 ; APPLICANT: Melloen, Robert
 ; APPLICANT: Puijk, Wouter
 ; APPLICANT: Schaaper, Wilhelms
 ; APPLICANT: Broekaert, Willem
 ; APPLICANT: Van Gelder, Wilhelms
 ; APPLICANT: Rees, Sarah
 ; TITLE OF INVENTION: Antifungal Proteins
 ; FILE REFERENCE: 50094PDDIV
 ; CURRENT APPLICATION NUMBER: US/10/388,361A
 ; CURRENT FILING DATE: 2003-03-13
 ; PRIOR APPLICATION NUMBER: US 09/077,948
 ; PRIOR FILING DATE: 1998-08-07
 ; PRIOR APPLICATION NUMBER: PCT/GB96/03068
 ; PRIOR FILING DATE: 1996-12-12
 ; PRIOR APPLICATION NUMBER: GB 9606552.9
 ; PRIOR FILING DATE: 1996-03-28

; PRIOR APPLICATION NUMBER: GB 9525455.3
 ; PRIOR FILING DATE: 1995-12-13
 ; NUMBER OF SEQ ID NOS: 141
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 45
 ; LENGTH: 414
 ; TYPE: DNA
 ; ORGANISM: Raphanus sativus
 ; US-10-388-361A-45

Query Match 100.0%; Score 414; DB 13; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.3e-101;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGTCTCTT 60
 Db 1 GTTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGTCTCTT 60
 QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
 Db 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
 QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
 Db 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
 QY 181 AACCTTGAGAAAGCAGCATGGATCTTGGCAACTTGTCCAGCTCACAAGTGTATC 240
 Db 181 AACCTTGAGAAAGCAGCATGGATCTTGGCAACTTGTCCAGCTCACAAGTGTATC 240
 QY 241 TGTACTTCTCTTCTTAACTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
 Db 241 TGTACTTCTCTTCTTAACTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
 QY 301 ACAAAATAGTCAGTGCACATCCATGAGTATTTTAAAGCATGTACAGATATGTTAT 360
 Db 301 ACAAAATAGTCAGTGCACATCCATGAGTATTTTAAAGCATGTACAGATATGTTAT 360
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

RESULT 3

US-10-006-252A-19
 ; Sequence 19, Application US/10006252A
 ; Publication No. US20020152498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Samblanx, Genevieve
 ; APPLICANT: Broekaert, Willem
 ; APPLICANT: Rees, Sarah
 ; TITLE OF INVENTION: Antifungal Proteins
 ; FILE REFERENCE: SYN-034DV
 ; CURRENT APPLICATION NUMBER: US/10/006,252A
 ; CURRENT FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 09/077,951
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: GB 9525474.4
 ; PRIOR FILING DATE: 1995-12-13
 ; PRIOR APPLICATION NUMBER: PCT/GB96/03065
 ; PRIOR FILING DATE: 1996-12-12
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 19
 ; LENGTH: 414
 ; TYPE: DNA
 ; ORGANISM: Raphanus sativus
 ; US-10-006-252A-19

Query Match 100.0%; Score 414; DB 14; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.3e-101;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGACATCTCTTTTGGTGTCTTT 60
Db 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGACATCTCTTTTGGTGTCTTT 60
QY 61 GTTCTTTTGTCTGTTTTCGAAGCACCAACAAATGTTGGAAGCAGAGTGTGCGAAAGG 120
Db 61 GTTCTTTTGTCTGTTTTCGAAGCACCAACAAATGTTGGAAGCAGAGTGTGCGAAAGG 120
QY 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACAAATTAACCCATGCAAGTATGTCATT 180
Db 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACAAATTAACCCATGCAAGTATGTCATT 180
QY 181 AACCTTGAGAAAGCACGACATGGAATCTTGCACATGATGTTCCAGCTCACAGTGTATC 240
Db 181 AACCTTGAGAAAGCACGACATGGAATCTTGCACATGATGTTCCAGCTCACAGTGTATC 240
QY 241 TGCTACTTCTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
Db 241 TGCTACTTCTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
QY 301 ACAAATAAGTCACTGTCACTATCCATGAGTGTATTTAGACATGTACAGATATGTTAT 360
Db 301 ACAAATAAGTCACTGTCACTATCCATGAGTGTATTTAGACATGTACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCCAAAAAATAAAAAAAAAAAAA 414
Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCCAAAAAATAAAAAAAAAAAAA 414

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RESULT 4

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US-09-759-584-58
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERPES, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..282
US-09-759-584-58

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Query Match 61.4%; Score 254.2; DB 9; Length 288;
Best Local Similarity 98.8%; Pred. No. 2.8e-58;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGACATCTCTTTTGGTGTCTTT 60
Db 28 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGACATCTCTTTTGGTGTCTTT 87
QY 61 GTTCTTTTGTCTGTTTTCGAAGCACCAACAAATGTTGGAAGCAGAGTGTGCGAAAGG 120
Db 88 GTTCTTTTGTCTGTTTTCGAAGCACCAACAAATGTTGGAAGCAGAGTGTGCGAAAGG 147
QY 121 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACAAATTAACCCATGCAAGTATGTCATT 180
Db 148 CCAAGTGGGACATGGTCAAGAGTCTGTGGAACAAATTAACCCATGCAAGTATGTCATT 207
QY 181 AACCTTGAGAAAGCACGACATGGAATCTTGCACATGATGTTCCAGCTCACAGTGTATC 240
Db 208 AGACTTGAGAAAGCACGACATGGAATCTTGCACATGATGTTCCAGCTCACAGTGTATC 267
QY 241 TGCTACTTCTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 259
Db 268 TGCTACTTCTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 286

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RESULT 5

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US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA AG Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699

```

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: PD1.1
STRAIN: PD1.1
US-09-732-561-13

Query March 58.6%; Score 242.4; DB 9; Length 403;
Best Local Similarity 76.5%; Pred. No. 5e-55;
Matches 297; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1 GTTTTATGATCATGCTAAGTTTGGTCCATCATCGGACCTCTTTTGGTCTCTT 60
DB 11 GTATAACAATAGTATGCTAAGTCTGCTACCATCGTTACTCTTTTCTTGGTCTCT 70
QY 61 GTTCTTTTGGTCTTTCGAAGCACCAACATGTTGGAAGCACAGAGTTTGTGCGAAGG 120
DB 71 GTTCTTTTGGTCTTTCGAAGCACCAACATGTTGGAAGCACAGAGTTTGTGCGAAGG 130
QY 121 CCAAGTGGACATGCTAGGAGTCTGTGGAACAATAACCATGCAAGATCATGTCATT 180
DB 131 CCAAGTGGACATGCTAGGAGTCTGTGGAACAATAACCATGCAAGATCATGTCATT 190
QY 181 AACCTTGAAAGACAGACATGATGTTGCAACTATGTTCCAGCTCACAGTGTATC 240
DB 191 AACCTTGAAAGACAGACATGATGTTGCAACTATGTTCCAGCTCACAGTGTATC 250
QY 241 TGCTACTTCCCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
DB 251 TGCTACTTCCCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTTAC 310
QY 301 ACAATATAGTCAGTCACATCATCCATGATGATTTTAAAGATGACAGATGTTAT 360
DB 311 CTATTAAATAGTATGTTCTACTCTATGAGAGTCTTATGACATGACAGATGTTAT 370
QY 361 GTTGTCTCGTTATACAAATAAAGTTT 388
DB 371 GTTGTCTCGTTATACAAATAAAGTTT 398

RESULT 6
US-09-732-561-15
Sequence 15, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Thomas, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Ag Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732.561
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: PD1.2
STRAIN: PD1.2
US-09-732-561-15

Query March 53.9%; Score 223; DB 9; Length 400;
Best Local Similarity 79.9%; Pred. No. 8.2e-50;
Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;
QY 5 TATTAGTATGATGCTAAGTTTGGTCCATCATCGGACCTCTTTTGGTCTCTTGTTC 64
DB 21 TATTATATCATGCTAAGTTTGTCTCCATCATCACCTTATCTTCGCTGCTCTTGTTC 80
QY 65 TTTTGTCTGCTTTTGAAGCACCAACAAATGTTGGAAGCACAGAGTTTGTGCGAAGCCAA 124
DB 81 TCTTTGTCTTTTGAAGCACCAACAAATGTTGGAAGCACAGAGTTTGTGCGAAGCCAA 140
QY 125 GTGGACATGTCAGGAGTCTGTGGAACAAATTAACCATGCAAGATCATGATTAACC 184
DB 141 GTGGACATGTCAGGAGTCTGTGGAACAAATTAACCATGCAAGATCATGATTAACC 200
QY 185 TTGAGAAAGCACGACATGATCTTGCACACTATGTTTCCAGCTCACAAGTGTATCTGT 244
DB 201 TTGAAGGAGCCCAACATGATCATGCAACTATGTTTCCAGCTCACAAGTGTATCTGT 260
QY 245 ACTTTCCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTATGTAATTTACAA 304
DB 261 ACGTCCCATGTTAAATCTTACCACCTAAATCTTTGGTGTAAATCGTGTATTTTACATAA 320
QY 305 AATAAGTCAGTCTCACTATCCATGATGATTTTAAAGACATGTA 347
DB 321 AATAAGTCAGTCTCAC--TCINTGAGTAACTTTATGACATGCA 361

RESULT 7
US-09-887-576-607
Sequence 607, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692

; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 875
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 607
 ; LENGTH: 400
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(400)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-887-576-607

Query Match 53.9%; Score 223; DB 9; Length 400;
 Best Local Similarity 79.9%; Pred. No. 8.2e-50;
 Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;
 QY 5 TATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGCTGCTTGTTC 64
 Db 21 TAATAATCATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGCTGCTTGTTC 80
 QY 65 TTTTGTGCTTTTGAAGCACCACAAATGTTGGAAGCACAAGAGTTGTGGAAAGCCAA 124
 Db 81 TCTTTGTGCTTTTCGACGCCCGGCAATGTTGGAAGCACAAGAGTTGTGGAAAGCCAA 140
 QY 125 GTGGGACATGTCAGGAGTCTGTGGAACAAATAGCGATGCAAGATCATGATTAACC 184
 Db 141 GTGGGACATGTCAGGAGTCTGTGGAACAAATAGCGATGCAAGATCATGATTAACC 200
 QY 185 TTGAAAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 244
 Db 201 TTGAAAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 260
 QY 245 ACTTTCCTGTTAATTTATTCGAACTCTTTGGTGAATAGTTTATGTAATTTACACAA 304
 Db 261 ACGTCCATGTTAATTTATTCGAACTCTTTGGTGAATAGTTTATGTAATTTACATAAA 320
 QY 305 AATAAGTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 347
 Db 321 AATAAGTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361

RESULT 8
 US-09-829-381A-16
 ; Sequence 16, Application US/09829381A
 ; Patent No. US20020144306A1
 ; GENERAL INFORMATION:

APPLICANT: Liang, Jihong
 Applicant: Shah, Dilip M.
 Wu, Yonnie S.
 Rosenberger, Cindy A.
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
 STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/829,381A
 FILING DATE: 09-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/103,489
 FILING DATE: 1998-06-24

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cohen, Charles E.
 ; REGISTRATION NUMBER: 34,565
 ; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 537-6224
 ; TELEFAX: (314) 537-6047
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 285 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "synthetic DNA"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-829-381A-16

Query Match 52.9%; Score 219; DB 9; Length 285;
 Best Local Similarity 90.3%; Pred. No. 8.2e-49;
 Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGCTGCTT 60
 Db 16 GTTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGCTGCTT 75
 QY 61 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCACAAGAGTTGTGGAAAGG 120
 Db 76 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCACAAGAGTTGTGGAGAGG 135
 QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAACAAATAGCGATGCAAGATCATGTCATT 180
 Db 136 CCATCAGGAGTCTGTGGAAGCACAAGAGTTGTGGAGAGTCTGTGGAAGCACAAGATGCATC 195
 QY 181 AACCTTGAGAAAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 196 AACCTTGAGAAAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 255
 QY 241 TGTACTTCTCTTGTGTTAAT 259
 Db 256 TGTACTTCTCTTGTGTTAAT 274

RESULT 9
 US-10-681-972-16
 ; Sequence 16, Application US/10681972
 ; Publication No. US20040064850A1
 ; GENERAL INFORMATION:

APPLICANT: Liang, Jihong
 Applicant: Shah, Dilip M.
 Wu, Yonnie S.
 Rosenberger, Cindy A.
 TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alysum and Methods for Co
 TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alysum and Methods for Co
 TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alysum and Methods for Co
 FILE REFERENCE: 38-21 (10700) C
 CURRENT APPLICATION NUMBER: US/10/681,972
 CURRENT FILING DATE: 2003-10-09
 PRIOR APPLICATION NUMBER: US/09/829,381D
 PRIOR FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 09/103,489
 PRIOR FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 285
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-10-681-972-16
 Query Match 52.9%; Score 219; DB 13; Length 285;
 Best Local Similarity 90.3%; Pred. No. 8.2e-49;

Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTCTTTTGGTCTCTT 60
 |||||
 Db 16 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTCTTTTGGTCTCTC 75
 |||||
 QY 61 GTTCTTTTGGTCTCTTGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAGG 120
 |||||
 Db 76 GTTCTCTTTTGGTCTCTTGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAGG 135
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 QY 121 CCAAGTGGGACATGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATT 180
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 Db 136 CCATCAGGACTTGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATT 195
 |||||
 QY 181 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
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 Db 196 AACCTCGAAGACAGGATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 255
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 QY 241 TGCTACTTTCTTGTAAAT 259
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 Db 256 TGCTACTTTCCATGCTAAT 274
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RESULT 10

US-09-829-381A-17

; Sequence 17, Application US/09829381A

; Patent No. US20020144306A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip M.

Wu, Yinnie S.

Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-829-381A-17

Query Match 52.1%; Score 215.8; DB 9; Length 285;

Best Local Similarity 89.6%; Pred. No. 5.9e-48;

Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTCTTTTGGTCTCTT 60
 |||||
 Db 16 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTCTTTTGGTCTCTC 75
 |||||
 QY 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAGG 120
 |||||
 Db 76 GTTCTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAGG 135
 |||||
 QY 121 CCAAGTGGGACATGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATT 180
 |||||
 Db 136 CCATCAGGACTTGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATT 195
 |||||
 QY 181 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
 |||||
 Db 196 AGACTCGAAGACAGGATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 255
 |||||
 QY 241 TGCTACTTTCTTGTAAAT 259
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 Db 256 TGCTACTTTCCATGCTAAT 274
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RESULT 11

US-10-681-972-17

; Sequence 17, Application US/10681972

; Publication No. US20040064850A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

Shah, Dilip M.

Wu, Yinnie S.

Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/681,972

FILING DATE: 2003-10-09

PRIOR APPLICATION NUMBER: US/09/829,381D

PRIOR FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 09/103,489

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patent in version 3.1

SEQ ID NO 17

TYPE: DNA

LENGTH: 285

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-681-972-17

Query Match 52.1%; Score 215.8; DB 13; Length 285;

Best Local Similarity 89.6%; Pred. No. 5.9e-48;

Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTCTTTTGGTCTCTT 60
 |||||
 Db 16 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTCTTTTGGTCTCTC 75
 |||||
 QY 61 GTTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAGG 120
 |||||
 Db 76 GTTCTCTTTTGGTCTCTTTCGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGCGAAGG 135
 |||||
 QY 121 CCAAGTGGGACATGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATT 180
 |||||
 Db 136 CCATCAGGACTTGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATT 195
 |||||
 QY 181 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
 |||||
 Db 196 AGACTCGAAGACAGGATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 255
 |||||
 QY 241 TGCTACTTTCTTGTAAAT 259
 |||||

Db
256 TGCTACTTTCCCATGCTAAT 274

RESULT 12

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US-09-829-381A-9
; Sequence 9, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Wu, Yonnie S.
; Rosenberger,
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi.

```

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/829,381A
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE TYPE: CDNA
US-09-829-381A-9

Db 299 CTTCCCATGTTAATCTACCAATCACATTTTGTGCTGTGTGATTTTACATGTTATG 358

Qy 290 ATGTAATTTACAAAATAAGTCAGTGCTCACTATCCATGAGTCATTTTTAAGACATGTACC 349

Db 359 TGTATTATTACATGAATAAGTCGTGTCA-TCCCTATGGTGACCTTATGACATGTACC 417

Qy 350 AGATATGTTAT-----GTTGGTGGGTTATACAATAAAGTTTTTATCACCAA 397

Db 418 AGATATATCATATGATGTGTTGTTTGTGTGGCAATTAAACTTTTATTGTGCA 477

Qy 398 AAAAAAAAAAAAAAAA 414

Db 478 TGCAAAAAAAAAAAAA 494

RESULT 13

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US-10-681-972-9
; Sequence 9, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yinnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAAPP from Alyssum and Methods for Co
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Alyssum spp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: N = any nucleotide
US-10-681-972-9

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:24:03 ; Search time 2517 Seconds
(without alignments)
4911.777 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 414

Sequence: 1 gttttattatgatcgtgc.....caaaaaaaaaaaaaaaaaaa 414

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum.*

3: em_estmu.*

4: em_estm.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estl.*

9: gb_estl.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_fod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	311	75.1	452	14	CD832071

5	310.6	75.0	519	14	CD835064
6	310	74.9	447	14	CD832592
7	309.4	74.7	408	14	CD833779
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15	307	74.2	438	14	CD831479
16	307	74.2	553	14	CD831014
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18	305.4	73.8	419	14	CD834168
19	305.4	73.8	421	14	CD833977
20	305.4	73.8	421	14	CD837517
21	303.8	73.4	453	14	CD834008
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23	302.2	73.0	422	14	CD831972
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26	275.2	66.5	449	14	CD833047
27	268.2	64.8	425	14	CD834852
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30	268	64.7	473	14	CD834995
31	266.6	64.4	427	14	CD833613
32	266.6	64.4	522	14	CD833938
33	266.6	64.4	543	14	CD830628
34	266.4	64.3	482	14	CD833627
35	265.4	64.1	476	14	CD833784
36	265.4	64.1	476	14	CD834092
37	264.8	64.0	481	14	CD833924
38	263.8	63.7	457	14	CD831226
39	263.8	63.7	457	14	CD831392
40	261.2	63.1	409	14	CD832294
41	260.2	62.9	646	14	CD829429
42	258.4	62.4	448	14	CD837568
43	255.6	61.7	543	14	CD829085
44	253.2	61.2	803	28	BH458392
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ALIGNMENTS

RESULT 1
LOCUS CD834994
DEFINITION CD834994 BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
ACCESSION CD834994
VERSION CD834994.1 GI:32516934
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 458)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.
FEATURES
source 1..458

CD834994 458 bp mRNA linear EST 10-JUL-2003
BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
sequence.

CD834994
CD834994.1
GI:32516934
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 458)

Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.
Location/Qualifiers
source 1..458

/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45043006"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Query Match 75.8%; Score 313.8; DB 14; Length 458;
Best Local Similarity 88.7%; Pred. No. 8.4e-42;
Matches 362; Conservative 0; Mismatches 43; Indels 3; Gaps 2;

Qy 1 GTTTTATAGTATGATCGCTTAAGTTTGGCTGCATCATCGCACTCTTTTGGCTGCTCTT 60
Db 51 GTATTACTAGTGAAGCAAGGCTTAAGTTTGGCTGCATCATCGCACTCTTTTGGCTGCTCTT 110
Qy 61 GTTCTTTTGGCTGCTTTTGAAGCACCACAAATGGTGGAAAGCAGAGAGTTGTGCGAAAGG 120
Db 111 GTTCTTTTGGCTGCTTTTGAAGCACCACAAATGGTGGAAAGCAGAGAGTTGTGCGAGAGG 170
Qy 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACCAATTAAGCATGCAAGATCAGTGCATT 180
Db 171 CCAAGTGGACATGGTCAGAGTCTGTGGAACCAATTAAGCATGCAAGATCAGTGCATT 230
Qy 181 AACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
Db 231 AACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 290
Qy 241 TGCTACTTCCCTGTTAACTTATCGCAAACTCTTTGGTGGTAAAGTTTATGTAATTTAC 300
Db 291 TGCTACTTCCCTGTTAACTTATCGCAAACTCTTTGGTGGTAAAGTTTATGTAATTTAC 350
Qy 301 ACAAATAGTCAGTGCATCTCCATGAGTATTTAAGACATGATCC--AGATATGTT 358
Db 351 ATAAATAGTCAGTGCATCTCCATGAGTATTTAAGACATGATCC--AGATATGTT 410
Qy 359 ATGTTGGTTCGGTTATCAAAATAGTTTATTCACCAAAAAA 406
Db 411 ATGTTGGTTCGGTTATCAAAATAGTTTATTCACCAAAAAA 457

RESULT 2

CD831680
LOCUS BN40.060H13F011227 BN40 Brassica napus cDNA clone BN40060H13, mRNA
DEFINITION

sequence.
CD831680.1 GI:32513620

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1. .470
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"

ORIGIN

/clone="BN40060H13"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN

Query Match 75.2%; Score 311.2; DB 14; Length 470;
Best Local Similarity 89.7%; Pred. No. 2.2e-41;
Matches 357; Conservative 0; Mismatches 38; Indels 3; Gaps 2;

Qy 1 GTTTTATAGTATGATCGCTTAAGTTTGGCTGCATCATCGCACTCTTTTGGCTGCTCTT 60
Db 73 GTATTACTAGTGAAGCAAGGCTTAAGTTTGGCTGCATCATCGCACTCTTTTGGCTGCTCTT 132
Qy 61 GTTCTTTTGGCTGCTTTTGAAGCACCACAAATGGTGGAAAGCAGAGAGTTGTGCGAAAGG 120
Db 133 GTTCTTTTGGCTGCTTTTGAAGCACCACAAATGGTGGAAAGCAGAGAGTTGTGCGAGAGG 192
Qy 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACCAATTAAGCATGCAAGATCAGTGCATT 180
Db 193 CCAAGTGGACATGGTCAGAGTCTGTGGAACCAATTAAGCATGCAAGATCAGTGCATT 252
Qy 181 AACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
Db 253 AACCTTGAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 312
Qy 241 TGCTACTTCCCTGTTAACTTATCGCAAACTCTTTGGTGGTAAAGTTTATGTAATTTAC 300
Db 313 TGCTACTTCCCTGTTAACTTATCGCAAACTCTTTGGTGGTAAAGTTTATGTAATTTAC 372
Qy 301 ACAAATAGTCAGTGCATCTCCATGAGTATTTAAGACATGATCC--AGATATGTT 358
Db 373 ATAAATAGTCAGTGCATCTCCATGAGTATTTAAGACATGATCC--AGATATGTT 432
Qy 359 ATGTTGGTTCGGTTATCAAAATAGTTTATTCACCA 396
Db 433 ATGTTGGTTCGGTTATCAAAATAGTTTATTCACCA 469

RESULT 3

LOCUS

CD834068
LOCUS BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
DEFINITION

sequence.

CD834068.1 GI:32516008

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES

source

1. .446
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040H17"
/tissue_type="seed"
/clone_lib="BN45"

Query Match 75.1%; Score 311; DB 14; Length 446;
 Best Local Similarity 89.2%; Pred. No. 2.5e-41;
 Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

Qy 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
 Db 51 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 114

Qy 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGGGAAGCAGAGTTGTGCGAAGG 120
 Db 111 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGGGAAGCAGAGTTGTGCGAAGG 170

Qy 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
 Db 171 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 230

Qy 181 AACCTTGGGAAGCAGACATGATCTTGGGAACAATAACGCATGCAAGAAATCAGTGCATT 240
 Db 231 AACCTTGGGAAGCAGACATGATCTTGGGAACAATAACGCATGCAAGAAATCAGTGCATT 290

Qy 241 TGTCTACTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 Db 291 TGTCTACTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 350

Qy 301 ACAAATAAGTCTAGTCTACTATCCATGAGTGAATTTTAAAGATGATGTTTATGTAATTTAC 358
 Db 351 ACAAATAAGTCTAGTCTACTATCCATGAGTGAATTTTAAAGATGATGTTTATGTAATTTAC 410

Qy 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
 Db 411 ATGTTGGTTCGGTTATACAAATAAAGTTT 439

RESULT 4
 CD832071
 LOCUS
 DEFINITION BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
 sequence.
 ACCESSION
 VERSION CD832071.1 GI:32514011
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 1 (bases 1 to 452)
 Genoplate.
 TITLE Genoplate, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplate
 Genoplate
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplate' (<http://www.genoplate.com>) and <http://genoplate-info.infobiogen.fr>.

FEATURES
 source
 Location/Qualifiers
 1..452
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40061003"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN
 Query Match 75.1%; Score 311; DB 14; Length 452;
 Best Local Similarity 89.2%; Pred. No. 2.4e-41;
 Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

Qy 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
 Db 51 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 110

Qy 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
 Db 55 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 114

Qy 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGGGAAGCAGAGTTGTGCGAAGG 120
 Db 115 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGGGAAGCAGAGTTGTGCGAAGG 174

Qy 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
 Db 175 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 234

Qy 181 AACCTTGGGAAGCAGACATGATCTTGGGAACAATAACGCATGCAAGAAATCAGTGCATT 240
 Db 235 AACCTTGGGAAGCAGACATGATCTTGGGAACAATAACGCATGCAAGAAATCAGTGCATT 294

Qy 241 TGTCTACTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 Db 295 TGTCTACTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 354

Qy 301 ACAAATAAGTCTAGTCTACTATCCATGAGTGAATTTTAAAGATGATGTTTATGTAATTTAC 358
 Db 355 ACAAATAAGTCTAGTCTACTATCCATGAGTGAATTTTAAAGATGATGTTTATGTAATTTAC 414

Qy 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
 Db 415 ATGTTGGTTCGGTTATACAAATAAAGTTT 443

RESULT 5
 CD835064
 LOCUS
 DEFINITION BN45.044C21F011228 BN45 Brassica napus cDNA clone BN45044C21, mRNA
 sequence.
 ACCESSION
 VERSION CD835064.1 GI:32517004
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 1 (bases 1 to 519)
 Genoplate.
 TITLE Genoplate, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplate
 Genoplate
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplate' (<http://www.genoplate.com>) and <http://genoplate-info.infobiogen.fr>.

FEATURES
 source
 Location/Qualifiers
 1..519
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45044C21"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN
 Query Match 75.0%; Score 310.6; DB 14; Length 519;
 Best Local Similarity 86.4%; Pred. No. 2.6e-41;
 Matches 355; Conservative 0; Mismatches 54; Indels 2; Gaps 1;

Qy 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
 Db 51 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 110

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QY 61 GTTCTTTTCTGCTTTTCGAAGCACCAAAATGGTGGAAAGCAGAGAAGTGTGCGAAAGG 120
Db 111 GTTCTTTTCTGCTTTTCGAAGCACCAAAATGGTGGAAAGCAGAGAAGTGTGCGAGAGG 170

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCCAAGATCAGTGCATT 180
Db 171 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCCAAGATCAGTGCATT 230

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
Db 231 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 290

QY 241 TGTACTTTCTGTTAAATTTATCGAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
Db 291 TGTACTTTCTGTTAAATTTATCGAAACTCTTTGGTGAATGTTTATGTAATTTAC 350

QY 301 ACAAATAAGTCAGTGCACATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
Db 351 ACAAATAAGTCAGTGCACATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 410

QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 409
Db 411 ATGTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAATA 461

RESULT 6
CD832592 447 bp mRNA linear EST 10-JUL-2003
LOCUS BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
DEFINITION sequence.
ACCESSION CD832592.1 GI:32514532
VERSION CD832592.1
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 447)
AUTHORS Genoplatte, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplatte
COMMENT Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
location/Qualifiers
1..447
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40063015"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match 74.9%; Score 310; DB 14; Length 447;
Best Local Similarity 88.9%; Pred. No. 3.6e-41;
Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

QY 1 GTTTTATAGTGCATGGCTAAGTTTGGTCCATCGCATCTTTTGTGCTCTT 60
Db 50 GTATTACTAGTGCATGGCTAAGTTTGGTCCATCGCATCTTTTGTGCTCTT 109

QY 61 GTTCTTTTCTGCTTTTCGAAGCACCAAAATGGTGGAAAGCAGAGAAGTGTGCGAAAGG 120
Db 110 GTTCTTTTCTGCTTTTCGAAGCACCAAAATGGTGGAAAGCAGAGAAGTGTGCGAGAGG 169

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QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCCAAGATCAGTGCATT 180
Db 170 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCCAAGATCAGTGCATT 229

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
Db 230 AACCTTGAGAAAGCAGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 289

QY 241 TGTACTTTCTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 300
Db 290 TGTACTTTCTGTTAAATTTATCGCAAACTCTTTGGTGAATGTTTATGTAATTTAC 349

QY 301 ACAAATAAGTCAGTGCACATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
Db 350 ACAAATAAGTCAGTGCACATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 409

QY 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
Db 410 ATGTTGGTTCGGTTATACAAATAAAGTTT 438

RESULT 7
CD833779 408 bp mRNA linear EST 10-JUL-2003
LOCUS BN45.001115F010914 BN45 Brassica napus cDNA clone BN45001115, mRNA
DEFINITION sequence.
ACCESSION CD833779
VERSION CD833779.1 GI:32515719
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 408)
AUTHORS Genoplatte, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplatte
COMMENT Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
location/Qualifiers
1..408
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45001115"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 74.7%; Score 309.4; DB 14; Length 408;
Best Local Similarity 88.9%; Pred. No. 4.8e-41;
Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

QY 1 GTTTTATAGTGCATGGCTAAGTTTGGTCCATCGCATCTTTTGTGCTCTT 60
Db 13 GTATTACTAGTGCATGGCTAAGTTTGGTCCATCGCATCTTTTGTGCTCTT 72

QY 61 GTTCTTTTCTGCTTTTCGAAGCACCAAAATGGTGGAAAGCAGAGAAGTGTGCGAAAGG 120
Db 73 GTTCTTTTCTGCTTTTCGAAGCACCAAAATGGTGGAAAGCAGAGAAGTGTGCGAGAGG 132

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCCAAGATCAGTGCATT 180
Db 133 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCCAAGATCAGTGCATT 192

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QY 181 AACCTTGAGAAAGCAGCATGGATCTTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
 Db 193 AACCTTGAGAAAGCAGCATGGATCTTTGCAACTATGCTTCCAGCTCACAAGTGTAT 252
 QY 241 TGCTACTTCCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTATTTTATGTAATTTAC 300
 Db 253 TGCTACTTCCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTATTTTATGTAATTTAC 312
 QY 301 ACAAAATAAGTCAGTGTCTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
 Db 313 ATAAATAAGTCTGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATGTT 372
 QY 359 ATGTTGGTTCGGTTATACAAATAAGTTT 387
 Db 373 ATGTTGGTTCGGTTATATAAAAGTTT 401

RESULT 8
 LOCUS CD834090
 DEFINITION BN45.040212F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA
 ACCESSION CD834090
 VERSION CD834090.1 GI:32516030
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 JOURNAL rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 COMMENT 1 (bases 1 to 409)

Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..409
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040121"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN
 Query Match 74.7%; Score 309.4; DB 14; Length 409;
 Best Local Similarity 88.9%; Pred. No. 4.7e-41;
 Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

QY 1 GTTTATTAGTATGATGCTAAGTTGGTCCATCATGCACTCTTTTGTGCTCTT 60
 Db 14 GTATTACTAGTGAAGTGGTAAAGTTGCTTCCATCATGCCCCACTTTTGTGCTCTT 73
 QY 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGTTGGAGACAGAAAGTTGCGAAAGG 120
 Db 74 GTTCTTTTGTCTTTTGAAGCACCACCAATGTTGGAGACAGAAAGTTGCGAGAGG 133
 QY 121 CCAAGTGGGACATGTCAGAGTCTGTGGAACAATACGATGCAAGATCAGTGCATT 180
 Db 134 CCAAGTGGGACATGTCAGAGTCTGTGGAACAATACGATGCAAGATCAGTGCATT 193
 QY 181 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTATC 240
 Db 194 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTAT 253

QY 241 TGCTACTTCCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTATTTTATGTAATTTAC 300
 Db 254 TGCTACTTCCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTATTTTATGTAATTTAC 313
 QY 301 ACAAAATAAGTCAGTGTCTATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
 Db 314 ATAAATAAGTCTGTGTCACTATCAATGAGTGAATTTTATGACATGTACCTGATATGTT 373
 QY 359 ATGTTGGTTCGGTTATACAAATAAGTTT 387
 Db 374 ATGTTGGTTCGGTTATATAAAAGTTT 402

RESULT 9
 LOCUS CD834611
 DEFINITION BN45.042H07F011228 BN45 Brassica napus cDNA clone BN45042H07, mRNA
 ACCESSION CD834611
 VERSION CD834611.1 GI:32516551
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 JOURNAL rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 COMMENT 1 (bases 1 to 450)

Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..450
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45042H07"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN
 Query Match 74.7%; Score 309.4; DB 14; Length 450;
 Best Local Similarity 88.9%; Pred. No. 4.4e-41;
 Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

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 Db 51 GTATTACTAGTGAAGTGGTAAAGTTGCTTCCATCATGCCCCACTTTTGTGCTCTT 110
 QY 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGTTGGAGACAGAAAGTTGCGAAAGG 120
 Db 111 GTTCTTTTGTCTTTTGAAGCACCACCAATGTTGGAGACAGAAAGTTGCGAGAGG 170
 QY 121 CCAAGTGGGACATGTCAGAGTCTGTGGAACAATACGATGCAAGATCAGTGCATT 180
 Db 171 CCAAGTGGGACATGTCAGAGTCTGTGGAACAATACGATGCAAGATCAGTGCATT 230
 QY 181 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTATC 240
 Db 231 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTAT 290
 QY 241 TGCTACTTCCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTATTTTATGTAATTTAC 300
 Db 291 TGCTACTTCCCTTGTTAATTTATCGCAACTCTTTGGTGAATAGTATTTTATGTAATTTAC 350


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QY 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
Db |||||||
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Db |||||||
QY 359 ATGTTGGTTTCGGTTATACAAATAAAGTTT 387
Db |||||||
QY 411 ATGTTGGTTTCGGTTATACAAATAAAGTTT 439
Db |||||||

RESULT 10
CD831294
LOCUS
DEFINITION
  BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
  sequence.
ACCESSION
  CD831294
VERSION
  CD831294.1 GI:32513234
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 438)
AUTHORS
  Genoplante, a major partnership french program in plant genomics
  Unpublished (2003)
JOURNAL
  Contact: Genoplante
COMMENT
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplante' (http://www.genoplante.com
  and http://genoplante-info.infobiogen.fr).
FEATURES
  source
  1..438
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    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN40058N13"
    /tissue_type="seed"
    /clone_lib="BN40"

ORIGIN
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  Best Local Similarity 90.6%; Pred. No. 6.1e-41;
  Matches 329; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATGATGGCTTAAGTTTGGCTCCATCATCGCACTCTTTTTCCTCTT 60
Db |||||||
QY 36 GTATTACTAGTATGATGGCTTAAGTTTGGCTCCATCATCGCACTCTTTTTCCTCTT 95
Db |||||||
QY 61 GTCTTTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 120
Db |||||||
QY 96 GTCTTTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 155
Db |||||||
QY 121 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCAATGCAAGTGTGCGAAT 180
Db |||||||
QY 156 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCAATGCAAGTGTGCGAAT 215
Db |||||||
QY 181 AACCTTGAAGAACGACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240
Db |||||||
QY 216 AACCTTGAAGAACGACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 275
Db |||||||
QY 241 TGCTACTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAT 300
Db |||||||
QY 276 TGCTACTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAT 335
Db |||||||
QY 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGAATTTAAGACATGTACCATATGTTAT 360
Db |||||||
QY 336 ATAAAAATAAGTCTGTGTCACTATCAATGAGTGAATTTATGACATGTACCTGATATGTTAT 395
Db |||||||

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QY 361 GTT 363
Db |||
QY 396 GTT 398
Db |||

RESULT 11
CD833944
LOCUS
DEFINITION
  BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
  sequence.
ACCESSION
  CD833944
VERSION
  CD833944.1 GI:32515884
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 420)
AUTHORS
  Genoplante, a major partnership french program in plant genomics
  Unpublished (2003)
JOURNAL
  Contact: Genoplante
COMMENT
  Genoplante
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplante' (http://www.genoplante.com
  and http://genoplante-info.infobiogen.fr).
FEATURES
  source
  1..420
  Location/Qualifiers
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    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN45040B07"
    /tissue_type="seed"
    /clone_lib="BN45"

ORIGIN
  Query Match 74.2%; Score 307; DB 14; Length 420;
  Best Local Similarity 90.4%; Pred. No. 1.1e-40;
  Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATGATGGCTTAAGTTTGGCTCCATCATCGCACTCTTTTTCCTCTT 60
Db |||||||
QY 35 GTATTACTAGTATGATGGCTTAAGTTTGGCTCCATCATCGCACTCTTTTTCCTCTT 94
Db |||||||
QY 61 GTCTTTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 120
Db |||||||
QY 95 GTCTTTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 154
Db |||||||
QY 121 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCAATGCAAGTGTGCGAAT 180
Db |||||||
QY 155 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCAATGCAAGTGTGCGAAT 214
Db |||||||
QY 181 AACCTTGAAGAACGACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 240
Db |||||||
QY 215 AACCTTGAAGAACGACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAGTGTATC 274
Db |||||||
QY 241 TGCTACTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAT 300
Db |||||||
QY 275 TGCTACTTTCCTCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAT 334
Db |||||||
QY 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTGAATTTAAGACATGTACCATATGTTAT 360
Db |||||||
QY 335 ATAAAAATAAGTCTGTGTCACTATCAATGAGTGAATTTATGACATGTACCTGATATGTTAT 394
Db |||||||
QY 361 GTT 363
Db |||
QY 395 GTT 397
Db |||

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RESULT 12

CD826491

LOCUS

CD826491 421 bp mRNA linear EST 10-JUL-2003
 BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA

DEFINITION

sequence.

ACCESSION

CD826491

VERSION

CD826491.1 GI:32508431

KEYWORDS

EST.

SOURCE

Brassica napus (rape)

ORGANISM

Brassica napus

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

AUTHORS

1 (bases 1 to 421)

TITLE

Genoplatte, a major partnership french program in plant genomics

JOURNAL

Unpublished (2003)

COMMENT

Contact: Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>and <http://genoplatte-info.infobiogen.fr>).

Location/Qualifiers

1..421

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet neuf"

/db_xref="taxon:3708"

/clone="BN25064A05"

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source

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/tissue_type="seed"

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source

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/organism="Brassica napus"

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/tissue_type="seed"

/clone_lib="BN25"

source

1..421

/organism="Brassica napus"

LOCUS

DEFINITION

CD833983

BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA

sequence.

CD833983

CD833983.1 GI:32515923

EST.

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 422)

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>and <http://genoplatte-info.infobiogen.fr>).

Location/Qualifiers

1..422

/organism="Brassica napus"

/mol_type="mRNA"

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/db_xref="taxon:3708"

/clone="BN45040D11"

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source

1..422

/organism="Brassica napus"

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/tissue_type="seed"

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1..422

/organism="Brassica napus"

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source

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source

1..422

/organism="Brassica napus"

/mol_type="mRNA"

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CD833983

BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA

sequence.

CD833983

CD833983.1 GI:32515923

EST.

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 422)

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Genoplatte

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Fax: 33 1 69 47 54 10

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plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>and <http://genoplatte-info.infobiogen.fr>).

Location/Qualifiers

1..422

/organism="Brassica napus"

/mol_type="mRNA"

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1..422

/organism="Brassica napus"

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/tissue_type="seed"

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source

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/organism="Brassica napus"

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/clone_lib="BN45"

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1..422

/organism="Brassica napus"

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/cultivar="Jet neuf"

/db_xref="taxon:3708"

/clone="BN45040D11"

CD833983

BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA

sequence.

CD833983

CD833983.1 GI:32515923

EST.

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 422)

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>and <http://genoplatte-info.infobiogen.fr>).

Location/Qualifiers

1..422

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Jet neuf"

/db_xref="taxon:3708"

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source

1..422

/organism="Brassica napus"

/mol_type="mRNA"

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/tissue_type="seed"

/clone_lib="BN45"

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1..422

/organism="Brassica napus"

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/tissue_type="seed"

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source

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/organism="Brassica napus"

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/db_xref="taxon:3708"

/clone="BN45040D11"

CD833983

BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA

sequence.

CD833983

CD833983.1 GI:32515923

EST.

Brassica napus (rape)

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 422)

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

VERSION CD827413.1 GI:32509353
 EST.
 KEYWORDS Brassica napus (rape)
 SOURCE
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 426)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Genoplante, a major partnership french program in plant genomics
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
 and <http://genoplante-info.infobiogen.fr>.

FEATURES
 source

1..426
 /organism="Brassica napus"
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 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN25067G02"
 /tissue_type="seed"
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ORIGIN

Query Match 74.2%; Score 307; DB 14; Length 426;
 Best Local Similarity 90.4%; Pred. No. 1.1e-40;
 Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATGCGACTTCCTTTTGGTCTCTT 60
 Db |||||
 Qy 61 GTTCTTTTGGTCTTTGGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGGAAGG 120
 Db |||||
 Qy 96 GTCTTTTGGTCTTTGGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGGAAGG 155
 Db |||||
 Qy 121 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATGTTGGAGACACAGAGTTGTCGGAAGG 180
 Db |||||
 Qy 156 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATGTTGGAGACACAGAGTTGTCGGAAGG 215
 Db |||||
 Qy 241 TGGTACTTCTCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 Db |||||
 Qy 276 TGGTACTTCTCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 335
 Db |||||
 Qy 301 ACAAAATAGTCAGTGTCTACTTCCATGAGTATTTAAGACATGTACCATATGTTAT 360
 Db |||||
 Qy 361 GTT 363
 Db |||||
 396 GTT 398

RESULT 15

CD831479
 LOCUS BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
 DEFINITION
 sequence.
 ACCESSION CD831479
 VERSION CD831479.1 GI:32513419
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 438)

Genoplante, a major partnership french program in plant genomics
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
 and <http://genoplante-info.infobiogen.fr>.

FEATURES
 source

1..438
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 /cultivar="Jet neuf"
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 /clone="BN40059J13"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Query Match 74.2%; Score 307; DB 14; Length 438;
 Best Local Similarity 90.4%; Pred. No. 1.1e-40;
 Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATGCGACTTCCTTTTGGTCTCTT 60
 Db |||||
 Qy 36 GTATTACTAGTATCATGGCTAAGTTTGGTCCATCATGCGACTTCCTTTTGGTCTCTT 95
 Db |||||
 Qy 61 GTTCTTTTGGTCTTTGGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGGAAGG 120
 Db |||||
 Qy 96 GTCTTTTGGTCTTTGGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGGAAGG 155
 Db |||||
 Qy 121 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATGTTGGAGACACAGAGTTGTCGGAAGG 180
 Db |||||
 Qy 156 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATGTTGGAGACACAGAGTTGTCGGAAGG 215
 Db |||||
 Qy 181 AACCTTGAGAAAGCAGACATGAGATCTTGCAACTATGCTTCCAGCTCACAAGTGATC 240
 Db |||||
 Qy 216 AACCTTGAGAAAGCAGACATGAGATCTTGCAACTATGCTTCCAGCTCACAAGTGATC 275
 Db |||||
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 Db |||||
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 Db |||||
 Qy 301 ACAAAATAGTCAGTGTCTACTTCCATGAGTATTTAAGACATGTACCATATGTTAT 360
 Db |||||
 Qy 361 GTT 363
 Db |||||
 396 GTT 398

Search completed: May 13, 2004, 10:53:14
 Job time : 2524 secs